

Gencore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 9, 2002, 12:03:31 : Search time 12 Seconds
(without alignments)
519.754 Million cell updates/sec

Title: US-09-786-926-1

Perfect score: 1966

Sequence: 1 NNATGTPVAPESCCQDLAAG.....RSLGPRMREPLSTISYSRSI 384

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 103943 seqs, 16242309 residues

Total number of hits satisfying chosen parameters: 103943

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published_Applications_AA:*
1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PC7_NEW_PUB.pep:*
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12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1966	100.0	384	9	US-09-971-228-10
2	1966	100.0	384	10	US-09-842-316-9
3	1966	100.0	384	10	US-09-731-030A-11
4	1966	100.0	384	12	US-10-007-399-1
5	1966	100.0	384	12	US-10-037-616-24
6	1956	99.5	384	10	US-09-731-030A-13
7	1948	99.1	384	10	US-09-827-937A-4
8	1642	83.5	386	10	US-09-917-508-2
9	993	50.5	224	10	US-09-731-030A-21
10	653	33.2	382	10	US-09-969-711-2
11	645.5	32.8	378	9	US-09-971-228-7
12	645.5	32.8	378	10	US-09-842-316-7
13	645.5	32.8	378	10	US-09-731-030A-18
14	645.5	32.8	378	12	US-10-037-616-21
15	645.5	32.8	398	10	US-09-815-333-2
16	645.5	32.8	398	10	US-09-842-316-2
17	645.5	32.8	398	12	US-10-037-616-26
18	640.5	32.6	362	10	US-09-993-844-8
19	638	32.5	400	9	US-09-971-228-12

20	638	32.5	400	10	US-09-812-272-2	Sequence 2, Appli
21	638	32.5	400	12	US-10-037-616-27	Sequence 27, Appl
22	635.5	32.3	341	9	US-09-971-228-13	Sequence 13, Appl
23	635.5	32.3	381	12	US-10-037-616-19	Sequence 19, Appl
24	635.5	32.3	381	10	US-09-971-228-5	Sequence 5, Appli
25	633	32.2	381	10	US-09-827-937A-18	Sequence 18, Appl
26	633	32.2	381	10	US-09-842-316-6	Sequence 6, Appli
27	633	32.2	381	10	US-09-731-030A-17	Sequence 17, Appl
28	627.5	31.9	346	9	US-09-971-228-15	Sequence 15, Appl
29	605	30.8	314	9	US-09-971-228-14	Sequence 14, Appl
30	535	27.2	353	10	US-09-731-030A-19	Sequence 19, Appl
31	534	27.2	353	10	US-09-771-063-2	Sequence 2, Appli
32	534	27.2	353	12	US-10-037-616-23	Sequence 23, Appl
33	526	26.8	353	9	US-09-971-228-9	Sequence 9, Appli
34	526	26.8	353	10	US-09-842-316-8	Sequence 8, Appli
35	520	26.4	353	10	US-09-771-063-4	Sequence 4, Appli
36	479.5	24.4	351	9	US-09-971-228-8	Sequence 8, Appli
37	479.5	24.4	351	12	US-10-037-616-22	Sequence 22, Appl
38	479.5	24.4	382	10	US-09-842-316-5	Sequence 5, Appli
39	450.5	22.9	348	10	US-09-903-799-2	Sequence 2, Appli
40	438	22.3	364	9	US-09-971-228-6	Sequence 6, Appli
41	438	22.3	364	10	US-09-842-316-3	Sequence 3, Appli
42	438	22.3	364	10	US-09-731-030A-15	Sequence 15, Appl
43	438	22.3	364	12	US-10-037-616-20	Sequence 20, Appl
44	425.5	21.6	354	10	US-09-879-225-2	Sequence 2, Appli
45	416.5	21.2	353	9	US-09-971-228-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1

US-09-971-228-10
Sequence 10, Application US/099711228
Patent No. US2002015512A1
GENERAL INFORMATION:
APPLICANT: Liao, X, Charlene
APPLICANT: Masuda, Sateban
APPLICANT: Chu, Peter
APPLICANT: Pardo, Jorge
APPLICANT: Li, Congfen
APPLICANT: Zhao, Haoran
APPLICANT: Jiang, Yiluying
APPLICANT: Rigel Pharmaceuticals, Incorporated
TITLE OF INVENTION: EDG: Modulators of Lymphocyte Activation and Migration
FILE REFERENCE: 021044-000310US
CURRENT APPLICATION NUMBER: US/09/971,228
CURRENT FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: US 60/284,763
PRIOR FILING DATE: 2001-04-18
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 10
LENGTH: 384
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: human endothelial differentiation G-protein
OTHER INFORMATION: coupled receptor (GPCR) 6 (EDG6)
US-09-971-228-10

Query Match 100.0%; Score 1966; DB 9; Length 384;

Best Local Similarity 100.0%; Pred. 1966; 5e-159; Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NNATGTPVAPESCCQDLAAGSHRLIVLHYNHSGRLAGRGEGDGLGALRGLSYAASCLV 60
DB 1 NNATGTPVAPESCCQDLAAGSHRLIVLHYNHSGRLAGRGEGDGLGALRGLSYAASCLV 60
QY 61 VLENLIVLAATSHMRKRWYCYLVNTLSDLTGAAYLANVLLSGARFRLPAQWFL 120
DB 61 VLENLIVLAATSHMRKRWYCYLVNTLSDLTGAAYLANVLLSGARFRLPAQWFL 120

QY 121 REGLLFTALAASTFSLFTAGERFATWVPVAESGATKTSRYVGTGICWLLAALLGMLP 180
DB 121 REGLLFTALAASTFSLFTAGERFATWVPVAESGATKTSRYVGTGICWLLAALLGMLP 180
QY 181 LLGNMCLCAFDRCSLLPLYSKRYILFCLVIFAGVLAITMGLYGAIFRLVQASGOKAPRP 240
DB 181 LLGNMCLCAFDRCSLLPLYSKRYILFCLVIFAGVLAITMGLYGAIFRLVQASGOKAPRP 240
QY 241 AARRKARRLKTVMLILAFVCMGPLEFGLLDADVFGSNLMAOEYLKGMWIIALAVLNS 300
DB 241 AARRKARRLKTVMLILAFVCMGPLEFGLLDADVFGSNLMAOEYLKGMWIIALAVLNS 300
QY 301 AVNPDIYSFRSREVCRAVLSFLCCGCLRLGMRGPGDCLARAWEHSGASTTDSLSLRPDS 360
DB 301 AVNPDIYSFRSREVCRAVLSFLCCGCLRLGMRGPGDCLARAWEHSGASTTDSLSLRPDS 360
QY 361 FRGSRSLSFRMRREPLSSISVSRSI 384
DB 361 FRGSRSLSFRMRREPLSSISVSRSI 384

RESULT 2

US-09-842-316-9
; Sequence 9, Application US/09842316
; Patent No. US20020099191A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENSIS, Eva
; APPLICANT: GASENHUBER, Johann
; TITLE OF INVENTION: EDG8 RECEPTOR, ITS PREPARATION AND USE
; FILE REFERENCE: 38005-147
; CURRENT APPLICATION NUMBER: US/09/842,316
; PRIOR FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: EP 116589.3
; PRIOR FILING DATE: 2000-08-01
; PRIOR APPLICATION NUMBER: EP 108858.2
; PRIOR FILING DATE: 2000-04-26
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 384
; TYPE: PRP
; ORGANISM: Homo sapiens
US-09-842-316-9

Query Match 100.0%; Score 1966; DB 10; Length 384;
Best Local Similarity 100.0%; Pred. No. 5e-159;

Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNATGTPVAPESCQQLAAGHSRLIVLHYNHSGLRAGRGPEDEGLGALRGISVAASCLV 60
DB 1 MNATGTPVAPESCQQLAAGHSRLIVLHYNHSGLRAGRGPEDEGLGALRGISVAASCLV 60
QY 61 VLENLVLAAITSHMRSRWYVYCLVNITLSDLTGAAYLANVLISGARTFRLAPQWFL 120
DB 61 VLENLVLAAITSHMRSRWYVYCLVNITLSDLTGAAYLANVLISGARTFRLAPQWFL 120
QY 121 REGLLFTALAASTFSLFTAGERFATWVPVAESGATKTSRYVGTGICWLLAALLGMLP 180
DB 121 REGLLFTALAASTFSLFTAGERFATWVPVAESGATKTSRYVGTGICWLLAALLGMLP 180
QY 181 LLGNMCLCAFDRCSLLPLYSKRYILFCLVIFAGVLAITMGLYGAIFRLVQASGOKAPRP 240
DB 181 LLGNMCLCAFDRCSLLPLYSKRYILFCLVIFAGVLAITMGLYGAIFRLVQASGOKAPRP 240
QY 241 AARRKARRLKTVMLILAFVCMGPLEFGLLDADVFGSNLMAOEYLKGMWIIALAVLNS 300
DB 241 AARRKARRLKTVMLILAFVCMGPLEFGLLDADVFGSNLMAOEYLKGMWIIALAVLNS 300
QY 301 AVNPDIYSFRSREVCRAVLSFLCCGCLRLGMRGPGDCLARAWEHSGASTTDSLSLRPDS 360
DB 301 AVNPDIYSFRSREVCRAVLSFLCCGCLRLGMRGPGDCLARAWEHSGASTTDSLSLRPDS 360
QY 361 FRGSRSLSFRMRREPLSSISVSRSI 384

DB 361 FRGSRSLSFRMRREPLSSISVSRSI 384

RESULT 3

US-09-731-030A-11
; Sequence 11, Application US/09731030A
; Patent No. US20020142375A1
; GENERAL INFORMATION:
; APPLICANT: MUNROE, Donald G.
; APPLICANT: GUPTA, Aswani K.
; APPLICANT: ZASTAWNY, Roman L.
; TITLE OF INVENTION: MAMMALIAN EDG-7 RECEPTOR HOMOLOGS
; FILE REFERENCE: 8074-0015
; CURRENT APPLICATION NUMBER: US/09/731,030A
; PRIOR FILING DATE: 1998-12-29
; PRIOR APPLICATION NUMBER: 60/070,184
; PRIOR FILING DATE: 1997-12-30
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 384
; TYPE: PRP
; ORGANISM: Homo sapiens
US-09-731-030A-11

Query Match 100.0%; Score 1966; DB 10; Length 384;
Best Local Similarity 100.0%; Pred. No. 5e-159;

Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNATGTPVAPESCQQLAAGHSRLIVLHYNHSGLRAGRGPEDEGLGALRGISVAASCLV 60
DB 1 MNATGTPVAPESCQQLAAGHSRLIVLHYNHSGLRAGRGPEDEGLGALRGISVAASCLV 60
QY 61 VLENLVLAAITSHMRSRWYVYCLVNITLSDLTGAAYLANVLISGARTFRLAPQWFL 120
DB 61 VLENLVLAAITSHMRSRWYVYCLVNITLSDLTGAAYLANVLISGARTFRLAPQWFL 120
QY 121 REGLLFTALAASTFSLFTAGERFATWVPVAESGATKTSRYVGTGICWLLAALLGMLP 180
DB 121 REGLLFTALAASTFSLFTAGERFATWVPVAESGATKTSRYVGTGICWLLAALLGMLP 180
QY 181 LLGNMCLCAFDRCSLLPLYSKRYILFCLVIFAGVLAITMGLYGAIFRLVQASGOKAPRP 240
DB 181 LLGNMCLCAFDRCSLLPLYSKRYILFCLVIFAGVLAITMGLYGAIFRLVQASGOKAPRP 240
QY 241 AARRKARRLKTVMLILAFVCMGPLEFGLLDADVFGSNLMAOEYLKGMWIIALAVLNS 300
DB 241 AARRKARRLKTVMLILAFVCMGPLEFGLLDADVFGSNLMAOEYLKGMWIIALAVLNS 300
QY 301 AVNPDIYSFRSREVCRAVLSFLCCGCLRLGMRGPGDCLARAWEHSGASTTDSLSLRPDS 360
DB 301 AVNPDIYSFRSREVCRAVLSFLCCGCLRLGMRGPGDCLARAWEHSGASTTDSLSLRPDS 360
QY 361 FRGSRSLSFRMRREPLSSISVSRSI 384
DB 361 FRGSRSLSFRMRREPLSSISVSRSI 384

RESULT 4

US-10-007-399-1
; Sequence 1, Application US/10007399
; Patent No. US20020115150A1
; GENERAL INFORMATION:
; APPLICANT: Glucksmann, Maria A.
; TITLE OF INVENTION: 14275 Receptor, A No. US20020115150A1el G-Protein Coupled Receptor Family
; FILE REFERENCE: 035800/169287
; CURRENT APPLICATION NUMBER: US/10/007,399
; CURRENT FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1

LENGTH: 384
TYPE: prt
ORGANISM: Homo sapiens
US-10-007-399-1

Query Match 100.0%; Score 1966; DB 12; Length 384;
Best Local Similarity 100.0%; Pred. No. 5e-159;
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNATGTPVAPESCOOLAAGSHSLIVLHYNHSGLAGRGPEDEGGIGALRGLSVAASCLV 60
DB 1 MNATGTPVAPESCOOLAAGSHSLIVLHYNHSGLAGRGPEDEGGIGALRGLSVAASCLV 60
QY 61 VLENLIVLAATISHMRSRRWYVCLVNTITSDLTGAAVLAVLNSGARTFRLAPQWFL 120
DB 61 VLENLIVLAATISHMRSRRWYVCLVNTITSDLTGAAVLAVLNSGARTFRLAPQWFL 120
QY 121 REGILFTALAASTFSLFTAGERFATWVRPAESGATKTSRYVGFGLCWLALALGMLP 180
DB 121 REGILFTALAASTFSLFTAGERFATWVRPAESGATKTSRYVGFGLCWLALALGMLP 180
QY 181 ILGWNCLAFDRCSLLPLYSKRYILFCLVIFAGVLATIMGLYGAIFRLVQASGOKAPRP 240
DB 181 ILGWNCLAFDRCSLLPLYSKRYILFCLVIFAGVLATIMGLYGAIFRLVQASGOKAPRP 240
QY 241 AARRKARRLKTYMLLAFVCMGPLEFGLLADVFSGNLMAOEYLRGMDMILALAVLNS 300
DB 241 AARRKARRLKTYMLLAFVCMGPLEFGLLADVFSGNLMAOEYLRGMDMILALAVLNS 300
QY 301 AVNPITYSFRSREVCRAVLSFLCCGCLRLGMRGPDCLARAVERAHSASTTDSLRPRS 360
DB 301 AVNPITYSFRSREVCRAVLSFLCCGCLRLGMRGPDCLARAVERAHSASTTDSLRPRS 360
QY 361 FRGSRSLSFRMRPLSSISVSRSI 384
DB 361 FRGSRSLSFRMRPLSSISVSRSI 384

RESULT 5
US-10-037-616-24
Sequence 24, Application US/10037616
Patent No. US20020123148A1

GENERAL INFORMATION:
APPLICANT: English, Denis
APPLICANT: Kovacs, Richard J.
APPLICANT: Rizzo, Maria T.
APPLICANT: Sliva, Daniel T.
TITLE OF INVENTION: Sphingolipid Compositions and Methods for Their Therapeutic Use
FILE REFERENCE: 7042-119
CURRENT APPLICATION NUMBER: US/10/037, 616
CURRENT FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: US 60/243,887
PRIOR FILING DATE: 2000-10-27
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn version 3.1
SEQ ID NO 24
LENGTH: 384
TYPE: prt
ORGANISM: Homo sapiens
US-10-037-616-24

Query Match 100.0%; Score 1966; DB 12; Length 384;
Best Local Similarity 100.0%; Pred. No. 5e-159;
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNATGTPVAPESCOOLAAGSHSLIVLHYNHSGLAGRGPEDEGGIGALRGLSVAASCLV 60
DB 1 MNATGTPVAPESCOOLAAGSHSLIVLHYNHSGLAGRGPEDEGGIGALRGLSVAASCLV 60
QY 61 VLENLIVLAATISHMRSRRWYVCLVNTITSDLTGAAVLAVLNSGARTFRLAPQWFL 120
DB 61 VLENLIVLAATISHMRSRRWYVCLVNTITSDLTGAAVLAVLNSGARTFRLAPQWFL 120

QY 121 REGILFTALAASTFSLFTAGERFATWVRPAESGATKTSRYVGFGLCWLALALGMLP 180
DB 121 REGILFTALAASTFSLFTAGERFATWVRPAESGATKTSRYVGFGLCWLALALGMLP 180
QY 181 ILGWNCLAFDRCSLLPLYSKRYILFCLVIFAGVLATIMGLYGAIFRLVQASGOKAPRP 240
DB 181 ILGWNCLAFDRCSLLPLYSKRYILFCLVIFAGVLATIMGLYGAIFRLVQASGOKAPRP 240
QY 241 AARRKARRLKTYMLLAFVCMGPLEFGLLADVFSGNLMAOEYLRGMDMILALAVLNS 300
DB 241 AARRKARRLKTYMLLAFVCMGPLEFGLLADVFSGNLMAOEYLRGMDMILALAVLNS 300
QY 301 AVNPITYSFRSREVCRAVLSFLCCGCLRLGMRGPDCLARAVERAHSASTTDSLRPRS 360
DB 301 AVNPITYSFRSREVCRAVLSFLCCGCLRLGMRGPDCLARAVERAHSASTTDSLRPRS 360
QY 361 FRGSRSLSFRMRPLSSISVSRSI 384
DB 361 FRGSRSLSFRMRPLSSISVSRSI 384

RESULT 6
US-09-731-030A-13
Sequence 13, Application US/09731030A
Patent No. US20020142375A1

GENERAL INFORMATION:
APPLICANT: MONROE, Donald G.
APPLICANT: GUPTA, Ashwani K.
APPLICANT: ZASTAWNY, Roman L.
TITLE OF INVENTION: MAMMALIAN EDG-7 RECEPTOR HOMOLOGS
FILE REFERENCE: 8074-0015
CURRENT APPLICATION NUMBER: US/09/731,030A
CURRENT FILING DATE: 1998-12-29
PRIOR APPLICATION NUMBER: 60/070,184
PRIOR FILING DATE: 1997-12-30
NUMBER OF SEQ ID NOS: 21
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 13
LENGTH: 384
TYPE: prt
ORGANISM: Homo sapiens
US-09-731-030A-13

Query Match 99.5%; Score 1956; DB 10; Length 384;
Best Local Similarity 99.5%; Pred. No. 3.5e-158;
Matches 382; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MNATGTPVAPESCOOLAAGSHSLIVLHYNHSGLAGRGPEDEGGIGALRGLSVAASCLV 60
DB 1 MNATGTPVAPESCOOLAAGSHSLIVLHYNHSGLAGRGPEDEGGIGALRGLSVAASCLV 60
QY 61 VLENLIVLAATISHMRSRRWYVCLVNTITSDLTGAAVLAVLNSGARTFRLAPQWFL 120
DB 61 VLENLIVLAATISHMRSRRWYVCLVNTITSDLTGAAVLAVLNSGARTFRLAPQWFL 120
QY 121 REGILFTALAASTFSLFTAGERFATWVRPAESGATKTSRYVGFGLCWLALALGMLP 180
DB 121 REGILFTALAASTFSLFTAGERFATWVRPAESGATKTSRYVGFGLCWLALALGMLP 180
QY 181 ILGWNCLAFDRCSLLPLYSKRYILFCLVIFAGVLATIMGLYGAIFRLVQASGOKAPRP 240
DB 181 ILGWNCLAFDRCSLLPLYSKRYILFCLVIFAGVLATIMGLYGAIFRLVQASGOKAPRP 240
QY 241 AARRKARRLKTYMLLAFVCMGPLEFGLLADVFSGNLMAOEYLRGMDMILALAVLNS 300
DB 241 AARRKARRLKTYMLLAFVCMGPLEFGLLADVFSGNLMAOEYLRGMDMILALAVLNS 300
QY 301 AVNPITYSFRSREVCRAVLSFLCCGCLRLGMRGPDCLARAVERAHSASTTDSLRPRS 360
DB 301 AVNPITYSFRSREVCRAVLSFLCCGCLRLGMRGPDCLARAVERAHSASTTDSLRPRS 360
QY 361 FRGSRSLSFRMRPLSSISVSRSI 384
DB 361 FRGSRSLSFRMRPLSSISVSRSI 384

Db 361 FRGSRLSFRMRPLSSSSSVRSI 384

RESULT 7

US-09-827-937A-4
 : Sequence 4, Application US/09827937A
 : Patent No. US20020052043A1
 : GENERAL INFORMATION:
 : APPLICANT: L1, Y1
 : APPLICANT: Ruben, Steven M.
 : TITLE OF INVENTION: Human G-Protein Coupled Receptors
 : FILE REFERENCE: 1488.1220003
 : CURRENT APPLICATION NUMBER: US/09/827, 937A
 : CURRENT FILING DATE: 2001-04-09
 : PRIOR APPLICATION NUMBER: 08/852, 824
 : PRIOR FILING DATE: 1997-05-07
 : NUMBER OF SEQ ID NOS: 18
 : SOFTWARE: PatentIn Ver. 2.0
 : SEQ ID NO 4
 : LENGTH: 384
 : TYPE: PRT
 : ORGANISM: Homo sapiens
 : US-09-827-937A-4

Query Match 99.1%; Score 1948; DB 10; Length 384;
 Best Local Similarity 99.0%; Pred. No. 1,7e-157;
 Matches 380; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNATGTPVAPESCQOLAAGSHRLIVLHYNHSRLAGRGCPEDGGLGALRGLSVAASCLV 60
 1 MNATGTPVAPESCQOLAAGSHRLIVLHYNHSRLAGRGCPEDGGLGALRGLSVAASCLV 60
 Db 1
 QY 61 VLENLVLAAITSHMRSRMVYICLVNTITSLDTGAAYLANVLSARFRLAPQWPL 120
 61 VLENLVLAAITSHMRSRMVYICLVNTITSLDTGAAYLANVLSARFRLAPQWPL 120
 Db 61
 QY 121 REGLEFALAASTFLFTAGRFATNVPVAESGATYTSRYVIGLQWLLAALGMDP 180
 121 REGLEFALAASTFLFTAGRFATNVPVAESGATYTSRYVIGLQWLLAALGMDP 180
 Db 121
 QY 181 LIGMNCACAFDRCSLLPLYSKRYILFCLVIFACVLTIMKLYAIFRLVQASGOKAPRP 240
 181 LIGMNCACAFDRCSLLPLYSKRYILFCLVIFACVLTIMKLYAIFRLVQASGOKAPRP 240
 Db 181
 QY 241 AARRKARRLKTYLMLLAFLVCMGPIFLGLLADVFGSNLMAOEYLRGMWILLAVLNS 300
 241 AARRKARRLKTYLMLLAFLVCMGPIFLGLLADVFGSNLMAOEYLRGMWILLAVLNS 300
 Db 241
 QY 301 AVNPITISFRSREVCRAVSLFCGGLRLGMRPGDCLARAVEAHSASTTDSLRPRDS 360
 301 AVNPITISFRSREVCRAVSLFCGGLRLGMRPGDCLARAVEAHSASTTDSLRPRDS 360
 Db 301
 QY 361 FRGSRLSFRMRPLSSSSSVRSI 384
 361 FRGSRLSFRMRPLSSSSSVRSI 384
 Db 361

RESULT 8

US-09-917-508-2
 : Sequence 2, Application US/09917508
 : Patent No. US20020137136A1
 : GENERAL INFORMATION:
 : APPLICANT: TSUI, Ping
 : TITLE OF INVENTION: Rat G Protein Coupled Receptor, EDG6
 : FILE REFERENCE: GP-70715
 : CURRENT APPLICATION NUMBER: US/09/917, 508
 : CURRENT FILING DATE: 2001-07-27
 : PRIOR APPLICATION NUMBER: 60/222, 259
 : PRIOR FILING DATE: 2000-07-31
 : NUMBER OF SEQ ID NOS: 2
 : SOFTWARE: FastSeq for Windows Version 3.0
 : SEQ ID NO 2
 : LENGTH: 386

: TYPE: PRT
 : ORGANISM: RAT
 : US-09-917-508-2

Query Match 83.5%; Score 1642; DB 10; Length 386;
 Best Local Similarity 82.1%; Pred. No. 1.2e-131;
 Matches 315; Conservative 29; Mismatches 33; Indels 2; Gaps 2;

QY 6 TPVAPESCQOLAAGSHRLIVLHYNHSRLAGRGCPED-GGLALRGLSVAASCLVLEN 64
 6 TPVAPESCQOLAAGSHRLIVLHYNHSRLAGRGCPED-GGLALRGLSVAASCLVLEN 64
 Db 8
 QY 65 LVLAAITSHMRSRMVYICLVNTITSLDTGAAYLANVLSARFRLAPQWPLRECL 124
 65 LVLAAITSHMRSRMVYICLVNTITSLDTGAAYLANVLSARFRLAPQWPLRECL 124
 Db 65
 QY 125 LFTALAASTFLFTAGRFATNVPVAESGATYTSRYVIGLQWLLAALGMDPFLGW 184
 125 LFTALAASTFLFTAGRFATNVPVAESGATYTSRYVIGLQWLLAALGMDPFLGW 184
 Db 125
 QY 185 NCLCAFDRCSSLLPLYSKRYILFCLVIFACVLTIMKLYAIFRLVQASGOKAPRPARR 244
 185 NCLCAFDRCSSLLPLYSKRYILFCLVIFACVLTIMKLYAIFRLVQASGOKAPRPARR 244
 Db 185
 QY 245 KARLLKTYLMLLAFLVCMGPIFLGLLADVFGSNLMAOEYLRGMWILLAVLNSAVNP 304
 245 KARLLKTYLMLLAFLVCMGPIFLGLLADVFGSNLMAOEYLRGMWILLAVLNSAVNP 304
 Db 245
 QY 305 IISFRRSREVCRAVSLFCGGLRLGMRPGDCLARAVEAHSASTTDSLRPRDSFRGS 364
 305 IISFRRSREVCRAVSLFCGGLRLGMRPGDCLARAVEAHSASTTDSLRPRDSFRGS 364
 Db 305
 QY 365 RSLSFRMRPLSSSSSVRS 383
 365 RSLSFRMRPLSSSSSVRS 383
 Db 365

RESULT 9

US-09-731-030A-21
 : Sequence 21, Application US/09731030A
 : Patent No. US20020142375A1
 : GENERAL INFORMATION:
 : APPLICANT: MONROE, Donald G.
 : APPLICANT: GUPTA, Ashwani K.
 : TITLE OF INVENTION: MAMMALIAN EDG-7 RECEPTOR HOMOLOGS
 : FILE REFERENCE: 8074-0015
 : CURRENT APPLICATION NUMBER: US/09/731, 030A
 : CURRENT FILING DATE: 1998-12-29
 : PRIOR APPLICATION NUMBER: 60/070, 184
 : PRIOR FILING DATE: 1997-12-30
 : NUMBER OF SEQ ID NOS: 21
 : SOFTWARE: PatentIn Ver. 2.0
 : SEQ ID NO 21
 : LENGTH: 224
 : TYPE: PRT
 : ORGANISM: Rattus sp.
 : US-09-731-030A-21

Query Match 50.5%; Score 993; DB 10; Length 224;
 Best Local Similarity 82.4%; Pred. No. 4.9e-77;
 Matches 182; Conservative 24; Mismatches 15; Indels 0; Gaps 0;

QY 161 RYVGFGLQWLLAALGMDPFLGWNCCLAFDRCSLLPLYSKRYILFCLVIFAGVLTATM 220
 161 RYVGFGLQWLLAALGMDPFLGWNCCLAFDRCSLLPLYSKRYILFCLVIFAGVLTATM 220
 Db 1
 QY 221 GLYGALFRVQASGOKAPRPARRKARLLKTYLMLLAFLVCMGPIFLGLLADVFGSNL 280
 221 GLYGALFRVQASGOKAPRPARRKARLLKTYLMLLAFLVCMGPIFLGLLADVFGSNL 280
 Db 221
 QY 281 MAOEYLRGMWILLAVLNSAVNPITISFRSREVCRAVSLFCGGLRLGMRPGDCLAR 340
 281 MAOEYLRGMWILLAVLNSAVNPITISFRSREVCRAVSLFCGGLRLGMRPGDCLAR 340
 Db 281

Matches 147; Conservative 55; Mismatches 133; Indels 13; Gaps 6;

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Qy 28 HNHSGRLAGGCGPEDGGIGALRGLSVAASCLVYLENNLLAATISMSRRMYCYLVN 87
    ||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 21 H7OYVGTAKGLAEASEGSTLTTPVLFVLCISFVLENNLMTAIWKKNNKHHRMFEFAGN 80
    ||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Qy 88 ITLSDLLGCAVLAANYLLSGARTFLRPAOMFLREGLEFTYLAASFSLFTAGREFATM 147
    :||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db 81 LACDLGLAGIAKYKNIMMIGKRTFSLPTPWFLREGSMFVALGASTCSLLATAIRHITM 140
    :||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
Qy 148 VAPVASEGATFSYVYGFGLGCMITLALGMLPLGNNCLGAPDRCSLTPYKSRYTF 207
    :::::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 141 IK-MRPYDANKRRRVLLIGKCMITLPTALDPLGNNCLNLPDOSTIPLPSKRYIAF 199
    :::::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Qy 208 CLVIFAGVLAITMGLYGAIFLRVQASGOKAPREPARARRRLTKVTMLILFLVYCWGP 267
    :||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db 200 CISIFITALVTIYLARVLYFYSSRSRKAANNNSERSMALLRTVYIVVSFICMGP 258
    :||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
Qy 268 FGLLIADVFGSNLAQVETLRGMDMILALVNLAVNPITYSFGRREVCRVAFSLQGGCL 327
    :||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db 260 FLEFLIIVD-ACRQOACPIFLKQMEIYALVNLNAMPYIYTLAKRKRRRFR-LVNCCL 317
    :||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
Qy 328 RLGMRGPDCLARVAEHSAGSTDDSLRPRDSFRGNSLSFRMRPEL 375
    :||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db 318 ---VGRG---ARRSPIDALDPs---RKSSSSSNHSHPKXEDL 355
    :||::||::||::||::||::||::||::||::||::||::||::||::||::||::||

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RESULT 13
US-09-731-030A-18

Sequence ID: US09-731-030A
Patent No.: US20020142375A1
GENERAL INFORMATION:
APPLICANT: MUNROE, Donald G.
APPLICANT: GUPTA, Ashwani K.
APPLICANT: ZASTAMNY, Roman L.
TITLE OF INVENTION: MAMMALIAN EDG-7 RECEPTOR HOMOLOGS
FILE REFERENCE: 8074-0015
CURRENT APPLICATION NUMBER: US/09/7731,030A
CURRENT FILING DATE: 1998-12-29
PRIOR APPLICATION NUMBER: 60/070,184
PRIOR FILING DATE: 1997-12-30
NUMBER OF SEQ. ID NOS.: 21
SOFTWARE: PatentIn Ver. 2.0
SEQ. ID NO.: 18
LENGTH: 378
TYPE: PRT
ORGANISM: Unknown
FEATURES:
OTHER INFORMATION: Description of Unknown Organism: Mammalian EDG

US-09-731-030A-18

Db 260 FILELIDV-ACRVQACPILFKAQWEIVLAVLSAMNPVITYTLASKEMRRAFER-LVCNCL 317

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QY      328  RLGNRGPGDCLARAVEAHSASTIDSSLRPDRSFRGSRSLFRMREPL 375
          :||| :| :| :| :|
Db      318  ---VGRG---ARASPIQPALPS---KSKSSSSNNSHSPKVKEDL 355
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RESULT 14
US-10-037-616-21
: sequence 21, Application US/10037616
: Patent No. US20020123148A1
: GENERAL INFORMATION:
: APPLICANT: English, Denis
: APPLICANT: Kovacs, Richard J.
: APPLICANT: Rizzo, Maria T.
: APPLICANT: Silva, Daniel T.
: TITLE OF INVENTION: Sphingolipid Compositions and Methods for Their Therapeutic Use
: FILE REFERENCE: 7042-119
: CURRENT APPLICATION NUMBER: US/10/037,616
: CURRENT FILING DATE: 2002-04-19
: PRIOR APPLICATION NUMBER: US 60/243,887
: PRIOR FILING DATE: 2000-10-27
: NUMBER OF SEQ. ID NOS: 27
: SOFTWARE: PatentIn version 3.1
: SEQ. ID NO. 21
: LENGTH: 378
: TYPE: PRT
: ORGANISM: Homo sapiens
US-10-037-616-21

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Query Match	32.8%	Score 645.5	DB 12	Length 378
Best Local Similarity	42.2%	Pred. N.2.1e-47		
Matches 147	Conservative 55	Mismatches 133	Indels 13	Gaps
QY	28	HYHNSGRLAGRGDEGGGALRGISVAASCLVYENLVLAATTSIMRSRRMYCYLVN	87	
Db	21	HYQYGRKGLAKEASEGGSTLTFTVPLVTCISFVLEINVLIAWKNNKHNRMYEFGAN	80	
QY	88	ITLSOLLGAAYLANVLGSGATTPRLAPACQFIRESLFPTLAASPSTLSIFPAGERFATM	147	
Db	81	IALCCLLAGIAIKYNVLINMGKRTFSLSPYTVFARBSMVNALGASTSLDAIAIRHILTM	140	
QY	148	VRPVAESQATKTSRYGFGICGLMLLAALDGMLEPLUGMNCICAFDRGSSLLPLYSKRYTLF	207	
Db	141	IK-MRPYDANKRRHRLVLTIGMCKMLIAFLCALDPLIGMNCINLPDGCSTIIPYSKRYTAF	199	
QY	208	CVIFAGVLAATIGLYGAIFRLVQASQOKAPREAPARRARRKLTVMILIAFLVYCQPL	267	
Db	200	CISIFPALTIVILYIARLYFVWSSSKKVAANNHNSRSMALLRTTVIVVYSFICQMSPL	259	

QY 268 FGLLLADVGSSNIMAOEYLRCMDMLIALAVNSANVPITISRSREVCRAVLSF
 Db 260 FILELIDV-ACRVOQACPILFRQOMFIVIALVNSAMPVITYTLASKEMRRAFR-L
 QY 328 RLMRPGCGCLRAAFAVHAHSGASTDSSLRLPRDSFRGSRSLSTPRMKEPL 375
 Db 318 ---VRGRG---ARASPIQPALDPs-----RSKSSSSNNSSHPKXYEDL 355
 RESULT 15
 US-09-815-333-2
 Sequence 2, Application US/09815333
 Patent No. US20010041335A1
 GENERAL INFORMATION:
 APPLICANT: Ramakrishnan, Shyam
 TITLE OF INVENTION: Regulation of Human Nerve Growth
 FILE REFERENCE: 04974, 00461
 CURRENT APPLICATION NUMBER: US/09/815,333
 CURRENT FILING DATE: 2001-03-23
 PRIOR APPLICATION NUMBER: 60/191,766
 PRIOR FILING DATE: 2000-03-24
 NUMBER OF SEQ ID NOS: 5

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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-815-333-2

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Query Match          32.8%; Score 645.5; DB 10; Length 398;
Best Local Similarity 40.8%; Pred. No. 2,2e-47;
Matches 154; Conservative 50; Mismatches 126; Indels 47; Gaps 7;

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QY 22 SRLIVLHYHNSGRLAGRGSPEDGGIGALRGLSVASCLVLENLVLAITSHMRSRRWV 81
    | : ||||| : : | : : : ||||| | : | :
Db 12 SEVIYVLYHYNTGKLRGARYQPGAGLRADAVVCIACAFIVLENLAVLVIGRHPFHAPM 71
    : | : ||||| ||||| ||||| | : ||||| | : ||||| |
QY 82 YYCLVNTLSDLTGAAYLANVLLSGARFERRAPQMFIREGLFTALASTFSLFTAG 141
    : | : ||||| ||||| ||||| | : ||||| | : ||||| |
Db 72 FLLLSGLTSLDLAGAAVADANILLSGPLTLKSPALMFAREGGVFVALTASVLSLIAIAL 131
    : | : ||||| ||||| ||||| | : ||||| | : ||||| |
QY 142 EREATWVR---PVASGATKTSRVYGFICWLLAALIGMLPLIGWNCLCAFDRCSLL 197
    | | | | | | : | : | : | : | : | : | : | : | : | :
Db 132 ERELTMARRGPAVSSRG-----RTLMAAAMGVSLILGLLPALGWNCLGRIDACSTYL 186
    | | | | | | | | | | | | | | | | | | | | | | | |
QY 198 PLYSKRYIIFCLVIFAGVLTATMGLYGAIFRLVQASGQKAP-RPA-----ARRKAR- 247
    ||| : | : ||| : | : ||| : | : ||| : | : ||| : | : ||| :
Db 187 PLYAKAYVLECYVAFVGIILAAICALYARIYCOVRANARLPPARPGTAGTSTRARRKPRS 246
    ||| : | : ||| : | : ||| : | : ||| : | : ||| : | : ||| :
QY 248 -RLTKTVLMIILAFVLCWGPFLFGLLLADYFGSNLMAQETLRGMWITLALAVLNSAVNPFI 306
    ||| : | : ||| : | : ||| : | : ||| : | : ||| : | : ||| :
Db 247 LALIKTLISVLLAFYACWGPFLFLLLLDVACPARTCPVILQA-DPFLGLAMANSLLNPFI 305
    ||| : | : ||| : | : ||| : | : ||| : | : ||| : | : ||| :
QY 307 YSFRSREVCRAVLSFLCCG-----CLRLGMRGPGDCLAR 340
    | : : | : | : | : | : | : | : | : | : | : | : | :
Db 306 YTLTNRDLRHALLRLVCCGRHSCGRDPSSGQGSASAAEASGGLRRCLPPGLDGSFSSSER 365
    | : : | : | : | : | : | : | : | : | : | : | : | :
QY 341 AVEAHSGASTDSSLRP 357
    : | : | : | : | : | : | : | : | : | : | : | : | :
Db 366 SSPQRDGLDTSGSTGSP 382
    : | : | : | : | : | : | : | : | : | : | : | : | :

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Search completed: December 9, 2002, 12:06:00
Job time : 13 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 9, 2002, 12:03:06 ; Search time 16 Seconds
(without alignments)
706.150 Million cell updates/sec

Title: US-09-786-926-1

Perfect score: 1966
Sequence: 1 MNATGTPVAPESCCQOLAAGC.....RSLSPFRMRPLSSISVSRSI 384

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- 1: Issued_Patents_AA.*
- 2: /cgn2_6/ptodata/1/1aa/5A.COMB.pep.*
- 3: /cgn2_6/ptodata/1/1aa/5B.COMB.pep.*
- 4: /cgn2_6/ptodata/1/1aa/6A.COMB.pep.*
- 5: /cgn2_6/ptodata/1/1aa/6B.COMB.pep.*
- 6: /cgn2_6/ptodata/1/1aa/6C.COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1948	99.1	384	US-08-852-824-4	Sequence 4, Appl
2	1437	73.1	509	US-08-845-566-1	Sequence 1, Appl
3	666	33.9	383	US-08-196-989B-4	Sequence 4, Appl
4	666	33.9	383	US-08-760-936-4	Sequence 2, Appl
5	653	33.2	382	US-09-542-733-2	Sequence 2, Appl
6	645.5	32.8	378	US-09-082-088-2	Sequence 2, Appl
7	645.5	32.8	378	US-09-546-117-2	Sequence 2, Appl
8	635.5	32.3	382	US-09-262-477-2	Sequence 2, Appl
9	633	32.2	381	US-08-845-566-3	Sequence 2, Appl
10	633	32.2	381	US-08-467-948A-28	Sequence 3, Appl
11	633	32.2	381	US-08-852-824-18	Sequence 28, Appl
12	633	32.2	381	US-08-467-947A-28	Sequence 28, Appl
13	633	32.2	381	PCT-US96-10618-4	Sequence 28, Appl
14	600	30.5	334	US-08-118-270-73	Sequence 4, Appl
15	600	30.5	334	PCT-US93-08528-73	Sequence 73, Appl
16	517.5	26.3	352	US-08-196-989B-2	Sequence 2, Appl
17	517.5	26.3	352	US-08-760-936-2	Sequence 2, Appl
18	479.5	24.4	351	US-08-789-982-2	Sequence 2, Appl
19	476.5	24.2	351	US-08-861-747-2	Sequence 2, Appl
20	444.5	22.6	364	US-08-763-938-2	Sequence 2, Appl
21	439	22.3	393	PCT-US96-10618-3	Sequence 2, Appl
22	434	22.1	364	PCT-US96-10618-2	Sequence 3, Appl
23	418	21.3	354	US-09-325-897-2	Sequence 2, Appl
24	418	21.3	354	US-09-837-726-2	Sequence 2, Appl
25	413.5	21.0	353	US-08-997-803-14	Sequence 14, Appl
26	334.5	17.0	213	US-08-997-803-15	Sequence 15, Appl
27	298	15.2	345	US-08-118-270-70	Sequence 70, Appl

28	298	15.2	345	PCT-US93-08528-70	Sequence 70, Appl
29	295.5	15.0	393	US-08-467-948A-4	Sequence 4, Appl
30	295.5	15.0	393	US-08-467-947A-4	Sequence 4, Appl
31	254	12.9	775	US-09-513-838-6	Sequence 6, Appl
32	248.5	12.6	362	US-09-513-838-2	Sequence 2, Appl
33	244.5	12.4	412	US-08-349-696-21	Sequence 21, Appl
34	244.5	12.4	412	US-08-233-009-21	Sequence 21, Appl
35	244.5	12.4	412	US-08-560-231-21	Sequence 21, Appl
36	244.5	12.4	412	US-09-080-704A-21	Sequence 21, Appl
37	240.5	12.2	325	US-08-387-805-16	Sequence 16, Appl
38	235	12.0	407	US-08-293-563-6	Sequence 6, Appl
39	228	11.6	572	US-08-334-698-2	Sequence 2, Appl
40	228	11.6	572	US-08-228-932-2	Sequence 2, Appl
41	228	11.6	572	US-08-468-939-2	Sequence 2, Appl
42	228	11.6	572	US-08-722-001-30	Sequence 30, Appl
43	228	11.6	572	US-08-406-855A-2	Sequence 2, Appl
44	228	11.6	572	US-08-722-190-2	Sequence 2, Appl
45	228	11.6	572	US-08-244-354-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-08-852-824-4
; Sequence 4, Application US/08852824C
; Patent No. 6060272
; GENERAL INFORMATION:
; APPLICANT: li et al.
; TITLE OF INVENTION: Human G-Protein Coupled Receptors
; FILE REFERENCE: 1488, 1220000
; CURRENT APPLICATION NUMBER: US/08/852, 824C
; CURRENT FILING DATE: 1997-05-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 4
; LENGTH: 384
; TYPE: PRT
; ORGANISM: genomic
US-08-852-824-4

Query Match	99.1%	Score 1948;	DB 3;	Length 384;
Best Local Similarity	99.0%	Pred. No. 4.1e-172;		
Matches 380;	Conservative 3;	Mismatches 1;	Indels 0;	Gaps 0;
QY	1	MNATGTPVAPESCCQOLAAGSHRLVLYHNSGRLAGRGPEDEGLGALRGLSVAAACIV	60	
DB	1	MNATGTPVAPESCCQOLAAGSHRLVLYHNSGRLAGRGPEDEGLGALRGLSVAAACIV	60	
QY	61	VLENTLVLAITSHMRBRWVYCIYVITLSDLTGAAYIANVLLSGARTFLAPQWFL	120	
DB	61	VLENTLVLAITSHMRBRWVYCIYVITLSDLTGAAYIANVLLSGARTFLAPQWFL	120	
QY	121	REGILFTALAASTFSLFTAGERFATWVRPAESGATKTSRYVGTGLCMLAALIGMPL	180	
DB	121	REGILFTALAASTFSLFTAGERFATWVRPAESGATKTSRYVGTGLCMLAALIGMPL	180	
QY	181	LLGNMNCACDRSSLLPLYSKRYILFCVITFAGVATITMGLYGAIFRLVQASGQKAPRP	240	
DB	181	LLGNMNCACDRSSLLPLYSKRYILFCVITFAGVATITMGLYGAIFRLVQASGQKAPRP	240	
QY	241	AARRKARRLKTYMLTILAFVCGPFLGILLADVGSNIMOXYLRGMDITLALVINS	300	
DB	241	AARRKARRLKTYMLTILAFVCGPFLGILLADVGSNIMOXYLRGMDITLALVINS	300	
QY	301	AVNPITYSFRSREVCAVSLFCCGCLRIGMRGPGDCLRAVEAHSASTTDSLRPRDS	360	
DB	301	AVNPITYSFRSREVCAVSLFCCGCLRIGMRGPGDCLRAVEAHSASTTDSLRPRDS	360	
QY	361	FRGSRSLSPFRMRPLSSISVSRSI 384		
DB	361	FRGSRSLSPFRMRPLSSISVSRSI 384		

RESULT 2

US-08-845-566-1
; Sequence 1, Application US/08845566
; Patent No. 5912144
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice
; APPLICANT: Guegler, Karl
; TITLE OF INVENTION: EDG-1 LIKE RECEPTOR
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/845,566
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0271 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 509 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: TYMNOR01
; CLONE: 144690
US-08-845-566-1

Query Match 73.1%; Score 1437; DB 2; Length 509;

Best Local Similarity 76.3%; Pred. No. 8,6e-125;

Matches 303; Conservative 8; Mismatches 42; Indels 44; Gaps 6;

OY 1 MNATGPVAPESCOQLAAGHSRLVLYHNHSGRLAGRGPEDEGGLGALRGLSVAASCLV 60
DB 1 MNATGPVAPESCOQLAAGHSRLVLYHNHSGRLAGRGPEDEGGLGALRGLSVAASCLV 60
OY 61 VLENLIVLAATITSHMSRWVYVCLVNTLSDLLTGAAYLANVLLSGARTFRLAPQWFL 120
DB 61 VLENLIVLAATITSHMSRWVYVCLVNTLSDLLTGAAYLANVLLSGARTFRLAPQWFL 120
OY 121 REGILFTALAASTFSLFTAGEFATWVRPVASGATKTSRYVGFGLCWLALLGMLP 180
DB 121 REGILFTALAASTFSLFTAGEFATWVRPVASGATKTSRYVGFGLCWLALLGMLP 180
OY 181 LLGMNCLCAFDRCSLLPYTSKRYILFCLVTFAGVATIMGLGAIFRLVQASGQKAPRP 240
DB 181 LLGMNCLCAFDRCSLLPYTSKRYILFCLVTFAGVATIMGLGAIFRLVQASGQKAPRP 240
OY 241 AARRKARRLKTVMLTLLAFVCMGPIFGILLADVFCSLMAQ----- 283
DB 241 AARRKARRLKTVMLTLLAFVCMGPIFGILLADVFCSLMAQ----- 283
OY 284 -EYLRGMDTLALAVLNSAVNPITYSPRSREVCRAVLSPFCGCGCLARMGKRGPDCLARAV 342
DB 284 -EYLRGMDTLALAVLNSAVNPITYSPRSREVCRAVLSPFCGCGCLARMGKRGPDCLARAV 342
OY 297 RPQLGGPQHLLLPQGGVGS-----RAQPSAAGVSGWAC-----EGPDCLARAV 343
DB 297 RPQLGGPQHLLLPQGGVGS-----RAQPSAAGVSGWAC-----EGPDCLARAV 343

OY 343 EAHSGASTDSDSLRPRDSRSLSPRMRPLSSIS 379
DB 344 EAHSGA-----SNHRQSLSEAKGQLS-----RLPLAQLS 371

RESULT 3

US-08-196-989B-4
; Sequence 4, Application US/08196989B
; Patent No. 5585476
; GENERAL INFORMATION:
; APPLICANT: MacLennan, A. John
; TITLE OF INVENTION: Molecular Cloning and Expression of
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: US
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/196,989B
; FILING DATE: 15-FEB-1994
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Lloyd, Jeff
; REGISTRATION NUMBER: 35,589
; REFERENCE/DOCKET NUMBER: MAC-100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 383 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-196-989B-4

Query Match 33.9%; Score 666; DB 1; Length 383;

Best Local Similarity 40.0%; Pred. No. 9.4e-54;

Matches 150; Conservative 69; Mismatches 126; Indels 30; Gaps 8;

OY 1 MNATGPVAPESCOQLAAGHSRLVLYHNHSGRLAGRGPEDEGGLGALRGLSVAASCLV 60
DB 2 VSSITIPVAKALRSQVSDYGVNVDIIVRHXYTGKL-NIGVEKDHGILKTSVFTLICLLI 60
OY 61 VLENLIVLAATITSHMSRWVYVCLVNTLSDLLTGAAYLANVLLSGARTFRLAPQWFL 120
DB 61 ILENFVLLTITWKTKKFRPMYVYFIGNLALSDLLAGVAYTANLLSGATVTKLTPAQWFL 120
OY 121 REGILFTALAASTFSLFTAGEFATWVRPVASGATKTSRYVGFGLCWLALLGMLP 180
DB 121 REGSFVVALSVSFTSLAIAIERITIMKMKLHNG-SNSSSFLLISACWVLSILGCLP 179
OY 181 LLGMNCLCAFDRCSLLPYTSKRYILFCLVTFAGVATIMGLGAIFRLVQASQ----- 235
DB 180 IGMNCCISSLSSCSVTLPLVHKHYILFCTVFTLLLSIVLYXCRIYSLVTRSRLLFR 239
OY 236 ----KAPRPARRRARRRLKTVMLTLLAFVCMGPIFGILLADVFCSLMAQ----- 291
DB 240 KNISRAAR-SSEKSLALKTVIIVLSYFIACMPLFILLDDV-GCKATCDILYKAEY 296
OY 292 IIALVLSAVNPITYSPRSREVCRAVLSPFCGCGCLARMGKRGPDCLARAVE 343
DB 297 FLVLAVLNSGPNPITYITLTKEMKRAFIIRITISCKCPKMGDSAGKFRPIIPGMFSR--- 353

Mon Dec 9 12:35:22 2002

us-09-786-926-1.rai

Page 4

```

ZIP: 19482
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/082,088
FILING DATE: 20-MAY-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Prestia, Paul F
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GP-70453
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
TELEFAX: 610-407-0701
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 378 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-082-088-2

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[illegible]

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: SEQ ID NO 2
: LENGTH: 378
:
: TYPE: PRT
: ORGANISM: HOMO SAPIENS
: US-09-546-117-2

Query Match      32.8%; Score 645.5; DB: 4; Length 378;
Best Local Similarity 42.2%; Pred. No. 7.2e-57;
Matches 14; Conservative 55; Mismatches 133; Indels 13; Gaps 6;

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Oy 28 HYHSGSLGRGPEDEGJGALRGISVAASCTIVENLTENLTIAATMSRRRRVVCVAV 87
Db 21 HYOYGVGLAORLKEABEGSTLTFTVLFYICSTIVLENLTIAATMKNNKRNHMYFFIGN 80
Oy 88 ITTSLDTLGAIVLANVLLSGAFTFRAPOMFLRBLGTLTALAASFSLFTNGERFATM 147
Db 81 LALCDLDTAGTAYVYNILMSGKRTFSLSPVTFELRGSMFVALGASTSLAIIEHHTM 140
Oy 148 VRPAESGAKTSTRVYGTGLCMLLAALGMLPLTGNNMCLCAFRCSSLPYVSKRYITF 207
Db 141 IK-MRPDANKRRHRRVFLLLGMCMLIAFTLFGAPLPLGMMCHLNPDCSTILPLYSKRTIAF 199
Oy 208 CVTYFACVLTATMGLTGATFRLVQASGOKAPRAPARRARRLKTYVMTLLTALVCKGFL 267
Db 200 CISTFTLITVLTIVLTARITFLVKSSSRVAVHNNNSESMALTTVYIVAVSEIACMSPL 259
Oy 268 FGLLADVFFSGNMAQEVLRGMWMLTALVLSAVNPITYFRRSEVRCRAVLFLLCCGL 327
Db 260 FILELLIDV-ACRYQACPIILFKAWOFLTALVLSANNPITYTLASKERBRAFFR-LVNCNCL 317
Oy 328 RLGRGPGDCLARAVERNHSASTTDSLSLRPRDSFRGSGSLSFRRKEPL 375
Db 318 ---VRGRG--ARASPIQALDPS-----RSKSSSSNNNSHSPKVEKPL 355

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01      1  MNATGTTPVAPESCCQILAGGHSRLIVLHYNHSGRAGRGCPEDGSLGALRGLSVAAASCLV 60
02
03      32.3%;      Score 635.5;  DB 4;      Length 382;
04      Best Local Similarity 40.5%;      Pred. No. 6,1e-51;
05      Matches 136;  Conservative 64;  Mismatches 121;  Indels 15;  Gaps 6;
06
07      US-09-262-477-2
08      RESULT 8
09      Sequence 2, Application US/09262477A
10      Patent No. 6423508
11      GENERAL INFORMATION:
12      APPLICANT: George Livt
13      APPLICANT: Derek Bergsma
14      APPLICANT: Jeffrey Stadel
15      APPLICANT: Winnie Chan
16      APPLICANT: Randall Wilson
17      APPLICANT: Shelagh Wilson
18      APPLICANT: Jon Chambers
19      APPLICANT: Philippe Robert
20      APPLICANT: Nassirah Khandoudi
21      TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDE SEQUENCES OF HUMAN EDG-1C AND
22      TITLE OF INVENTION: METHODS OF SCREENING FOR AGONISTS AND ANTAGONISTS FOR HUMAN
23      TITLE OF INVENTION: EDG-1C RECEPTOR AND SPHINGOSINE 1-PHOSPHATE LIGAND AND
24      TITLE OF INVENTION: INTERACTION THEREOF
25      FILE REFERENCE: G950006
26      CURRENT APPLICATION NUMBER: US/09/262,477A
27      CURRENT FILING DATE: 1999-03-04
28      EARLIER APPLICATION NUMBER: 1999-077,369
29      EARLIER FILING DATE: 1998-03-09
30      EARLIER APPLICATION NUMBER: 60/087,102
31      EARLIER FILING DATE: 1998-05-28
32      NUMBER OF SEQ. ID NOS.: 2
33      SOFTWARE: FastSeq for Windows Version 3.0
34      SEQ. ID NO. 2
35      LENGTH: 382
36      TYPE: PRT
37      ORGANISM: Human
38      US-09-262-477-2

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Db 1 MGPTSVPLVKAHRSVSDVYNDIVRHVNTGKL-NISADKENSIKLTSVFEILICCFI 59
QY 61 VLENLLVLAITSHMRSRRWYCCVNTLSDLLTGAAYLANVLISGARTRLAPAOQWL 120
Db 60 ILENIFVLLTIWTKRKHRRPMYFIGNLALSDLLAGAVAYANLLISGATTYKLTTPAOQWL 119
QY 121 REGLLFTALASTFSLFTAGERPAWVPVASEGATKTSRYGFGICWLLAALLGMLP 180
Db 120 REGSMFVALSASFELALAIERYITMLKMKLHNG-SNNRFLFLISACWVLSLILGSLP 178
QY 181 LIGMNCIAFDRCSSLLPLYSKRYLLFCLVTFAGVLTATMGLYGAIFRLVOASGQ----- 235
Db 179 IMGWNCISALSSCSTVPLDLYHKHYLLFCTVTFETLLSLIVLYCRISLVTRRSRLTFR 238
QY 236 ----KAPPRARKRRLKTYMLLAFVCMGPFELLLADVPGSNMAOEYLRGMW 291
Db 239 KNISKASR--SEKSLALKTVIIVLSVFIACWAPLFIILLLDV-GCKVKTCIDILFRAEY 295
QY 292 ILALAVNSAVNPITYSFRSREVCRAVLSFL-CCGC 326
Db 296 FLVLAVNSGTPNPIYTLTKEMRAAFIRIMSCCKC 331

RESULT 9

US-08-845-566-3
; Sequence 3, Application US/08845566
; Patent No. 5912144
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice
; APPLICANT: Guegler, Karl
; TITLE OF INVENTION: EDG-1 LIKE RECEPTOR
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/845,566
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0271 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-845-4166
; TELEFAX: 415-845-0555
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 361 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: Genbank
; CLONE: 181948
; US-08-845-566-3

Query Match 32.2%; Score 633; DB 2; Length 381;
Best Local Similarity 40.5%; Pred. No. 1e-50;
Matches 135; Conservative 63; Mismatches 125; Indels 10; Gaps 5;

QY 1 MNATGPVAPESQOQLAAGHSRLIVLHNHSGRLAGRGPEDEGICGLGLSVASCLV 60
Db 1 MGPTSVPLVKAHRSVSDVYNDIVRHVNTGKL-NISADKENSIKLTSVFEILICCFI 59
QY 61 VLENLLVLAITSHMRSRRWYCCVNTLSDLLTGAAYLANVLISGARTRLAPAOQWL 120
Db 60 ILENIFVLLTIWTKRKHRRPMYFIGNLALSDLLAGAVAYANLLISGATTYKLTTPAOQWL 119
QY 121 REGLLFTALASTFSLFTAGERPAWVPVASEGATKTSRYGFGICWLLAALLGMLP 180
Db 120 REGSMFVALSASFELALAIERYITMLKMKLHNG-SNNRFLFLISACWVLSLILGSLP 178
QY 181 LIGMNCIAFDRCSSLLPLYSKRYLLFCLVTFAGVLTATMGLYGAIFRLVOASGQAKAPP 240
Db 179 IMGWNCISALSSCSTVPLDLYHKHYLLFCTVTFETLLSLIVLYCRISLVTRRSRLTFR 238
QY 241 AARRKRR-----LKTVMILIAFLVCMGPFELLLADVPGSNMAOEYLRGMWILA 294
Db 239 KNISKASRSEBNVALLKTVIIVLSVFIACWAPLFIILLLDV-GCKVKTCIDILFRAEYFLV 297
QY 295 LAVYNSAVNPITYSFRSREVCRAVLSFL-CCGC 326
Db 298 LAVYNSGTPNPIYTLTKEMRAAFIRIMSCCKC 330

RESULT 10

US-08-467-948A-28
; Sequence 28, Application US/08467948A
; Patent No. 5998164
; GENERAL INFORMATION:
; APPLICANT: LI, YI
; APPLICANT: CAO, LIANG
; APPLICANT: NI, JIAN
; APPLICANT: GENTZ, REINER
; APPLICANT: BULT, CAROL J.
; APPLICANT: SUTTON III, GRANGER G.
; TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVE., NW, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,948A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04079
; FILING DATE: 30-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.1140003/EKS/KLM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2540
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 381 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide

Dh 179 IMGWNCISALSSCSTVPLVHKHIIIFCTVFTLLLSLIIYICRIYSLVTRSRRLTR 238
Qy 241 AARRRARR-----LTKTYLMLLAFVCGPFLGILLADVFSGNMAOEYLRGMDWLLA 294
Dh 239 KNISKASRSSENVALLTKTYIIVLSVFIACWAPFLILLLDV-GCKVKTCDILFRAEYFLV 297
Qy 295 LAVNSAVNPITISFRSREVCRAVLSFL-CCGC 326
Dh 298 LAVNSGNTPIITYTLTKEMKRAFRIRMSCCKC 330

RESULT 13

PCT-US96-10618-4
; Sequence 4, Application PC/TUS9610618
; GENERAL INFORMATION:
; APPLICANT: Coleman, Roger
; APPLICANT: Guegler, Karl J.
; APPLICANT: Au-Young, Janice
; APPLICANT: Bandman, Olga
; APPLICANT: Selbhamer, Jeffrey J.
; TITLE OF INVENTION: A NOVEL HUMAN EDG-2 RECEPTOR HOMOLOG
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10618
; FILING DATE: 20-JUN-1996
; CLASSIFICATION:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 60/000,352
; FILING DATE: 20-JUN-1995
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/567,817
; FILING DATE: 06-DEC-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Glaister, Debra J.
; REGISTRATION NUMBER: 33,888
; REFERENCE/DOCKET NUMBER: PF-0042 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 381 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 119130
; PCT-US96-10618-4

Query Match 32.2%; Score 633; DB 5; Length 381;

Best Local Similarity 40.5%; Pred. No. 1e-50;

Matches 135; Conservative 63; Mismatches 125; Indels 10; Gaps 5;

Qy 1 MNATGPPVAESCGQLAAGSHRLIVLHNHSGRLARGSGPEDGGGLGALRGSLVAASCLV 60
Dh 1 MGPISVPLVAHRSVSVDYVNIIDIVRHVYTKL-NISADKENSIKLISVFIILCCET 59
Qy 61 VLENLVLAAITSHMSRRWVYCLVNTLSDLLTGAAVLAVNLGSGARTFRLAPAWFL 120

Dh 60 ILENIEFVLTITWKTKRHRPMYFIGNLALSDLLAGVAATANLLSGATTYKLTLPQWFL 119
Qy 121 REGILFALAASTFSLFTGERFATWVRVPAASGATKTSRVYGFGLCMLALLGMP 180
Dh 120 REGSMFVALASVSFLAIAIERITMLKMKLNG-SNNFRLLLSACWVLSLIGGLP 178
Qy 181 ILGNWNCIARDRCSSLLPIYSKRYILEFCIVFAGVLAITMGILGAIFFRLVOASGOKAPP 240
Dh 179 IMGWNCISALSSCSTVPLVHKHIIIFCTVFTLLLSLIIYICRIYSLVTRSRRLTR 238
Qy 241 AARRRARR-----LTKTYLMLLAFVCGPFLGILLADVFSGNMAOEYLRGMDWLLA 294
Dh 239 KNISKASRSSENVALLTKTYIIVLSVFIACWAPFLILLLDV-GCKVKTCDILFRAEYFLV 297
Qy 295 LAVNSAVNPITISFRSREVCRAVLSFL-CCGC 326
Dh 298 LAVNSGNTPIITYTLTKEMKRAFRIRMSCCKC 330

RESULT 14

US-08-118-270-73
; Sequence 73, Application US/08118270
; Patent No. 5508384
; GENERAL INFORMATION:
; APPLICANT: Murphy, Randall B.
; APPLICANT: Schuster, David I.
; TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
; NUMBER OF SEQUENCES: 348
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/118,270
; FILING DATE: 09-SEP-1993
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 07/943,236
; FILING DATE: 10-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Townsend, Kevin G.
; REGISTRATION NUMBER: 34,033
; REFERENCE/DOCKET NUMBER: MURPHY-2A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 73:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 334 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-118-270-73

Query Match 30.5%; Score 600; DB 1; Length 334;

Best Local Similarity 44.2%; Pred. No. 9.9e-48;

Matches 122; Conservative 53; Mismatches 91; Indels 10; Gaps 4;

Qy 58 CLVLENTLVLAATIRSHMSRRWVYCLVNTLSDLLTGAAVLAVNLGSGARTFRLAPAQ 117
Dh 11 CFIILENFVLTITWKTKRHRPMYFIGNLALSDLLAGVAATANLLSGATTYKLTLPQ 70

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 9, 2002, 12:03:06 ; Search time 21 Seconds
(without alignments)
1757.887 Million cell updates/sec

Title: US-09-786-926-1

Perfect score: 1966

Sequence: 1 MNATGTPVAPESCOQLAAG.....RSLSPKREPLSSISVSRSI 384

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database :

1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	666	33.9	383	2	153870
2	656.5	33.4	362	2	UC7559
3	645.5	32.8	378	2	JC5245
4	633	32.2	381	2	A35300
5	517.5	26.3	352	2	JC1465
6	438	22.3	364	2	JC5293
7	351	17.9	473	2	A33117
8	344.5	17.5	180	2	E48909
9	333	16.9	472	2	S17595
10	299.5	15.2	330	2	A55689
11	288.5	14.7	330	2	S40454
12	285	14.5	347	2	S70364
13	278.5	14.2	360	2	S36750
14	248.5	12.6	362	2	I65990
15	245	12.5	363	2	D30341
16	244.5	12.4	412	2	A48978
17	244.5	12.4	409	2	I48095
18	240.5	12.4	325	2	JN0764
19	237.5	12.1	325	2	JC5592
20	235	11.9	361	2	B46137
21	233.5	11.6	409	2	S68247
22	228.5	11.6	572	2	I39369
23	227.5	11.6	355	2	S39028
24	222	11.3	372	2	I49008
25	221.5	11.2	501	2	JH0447
26	221	11.2	314	2	S71420
27	221	11.2	314	2	S70005
28	221	11.2	314	2	S70005
29	221	11.2	314	2	S70005

30	220	11.2	387	2	S55550	5-HT4s receptor -
31	220	11.2	406	2	S55549	serotonin 4 recept
32	216.5	11.0	317	2	S45708	MSH receptor - bov
33	215	10.9	325	2	JC2193	melanocortin recep
34	215	10.9	351	1	A55962	opsin, pineal gland
35	214	10.9	352	1	I50081	rhodopsin - green
36	213.5	10.9	348	1	S23398	rhodopsin - Chinese
37	212.5	10.8	348	1	JC4267	opsin - rabbit
38	212	10.7	348	1	QO80	rhodopsin - bovine
39	211	10.7	560	2	A38731	alpha-1A adrenergic
40	210.5	10.7	320	2	S17177	probable G protein
41	208	10.6	332	2	I48933	adenosine receptor
42	207.5	10.6	332	2	A57055	melanocortin recep
43	207.5	10.6	348	1	S51677	rhodopsin - rat
44	207.5	10.6	348	1	QO8H	rhodopsin - sheep
45	207	10.5	332	2	JC1229	adenosine receptor

ALIGNMENTS

RESULT 1

Edg-1 Orphan receptor - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 29-May-1998 #sequence_revision 29-May-1998 #ext_change 24-Sep-1999

C:Accession: I53870

R:Lado, D.C.; Browe, C.S.; Gaskin, A.A.; Borden, J.M.; MacLennan, A.J.

Gene 149, 331-336, 1994

A:Title: Cloning of the rat edg-1 immediate-early gene: expression pattern suggests d

A:Reference number: I53870; M0ID:95047498; PMID:7959012

A:Accession: I53870

A>Status: preliminary; translated from GB/EMBL/DBD

A:Molecule type: mRNA

A:Residues: 1-383 <RES>

A:Cross-references: EMBL:U010303; NID:9595396; PIDN:AAA83418.1; PID:9595397

C:Superfamily: G protein-coupled receptor edg-1

Query Match 33.9% Score 666; DB 2: Length 383;

Best Local Similarity 40.0%; Pred. No. 3e-50;

Matches 150; Conservative 69; Mismatches 126; Indels 30; Gaps 8;

QY	1	MNATGTPVAPESCOQLAAGHSRLIVLHNSGRLAGRGSPEDGGLGALRGLSVAA	60
DB	2	VSSISIPVYKALRSQVEDYGNVDIVRHNYTGKL-NIGVEKHGKITLSVVFILCCL	60
QY	61	VLENLVLIAITSHMRSRMYVYCLVNTLSDLITGAAYLANVLSCARTFRLAPQWFL	120
DB	61	ILENIFVLLITMKTKKFRPMYVYIGNLALSDLAGVAYANLILSGATTYKILTPAQWFL	120
QY	121	REGILFTPLASTSTSLFTTGERFATWVRPAESGATKTSRVYGFGLCWLLAALGMP	180
DB	121	REGSFEVALSASFSLALAIERTITMKKLHNG-SNSRSFLLISACWVISLILGLP	179
QY	181	LLGNMCLAFDRCSLLPLYSKRYILFCVLVFAVATLIMGLYCAIRLYVQASQ----	235
DB	180	IMGNMCLISLSSCTVPLVYHKHYILFCVTFLLLSYLVCRIVSLVTRSRRLTFR	239
QY	236	---KAPPAARKRRLKTLVMTLLAFVYCWGPIELGLIADYFGSNLMAOELRMDW	291
DB	240	KNISAKSR--SSEKSLALIKTVIVLSVFIACMPFLTLLLDV-GCKARTCDILYAEY	296
QY	292	ILALAVLSAVNPITPSFRSREVCRAVLSFL-CCGCLRLGMRG-----PGDCLARAVE	343
DB	297	FLVALVLSGNPIIYITLTKEMKRAFRITISCKCRNGDSAGKFKRPIIPGMFSR---	353
QY	344	AHSGASTDSSLRPR 358	
DB	354	-----SKSDNSHPQ 363	

RESULT 2

JC7559

sphingosine 1-phosphate receptor - zebra fish
 N:Alternate names: endothelial differentiation gene 1 receptor.
 C:Species: Brachydanio rerio (zebra fish)
 C:Date: 30-Jun-2001 #sequence_reviston 30-Jun-2001 #text_change 03-Aug-2001
 C:Accession: J07559
 R:Im, D.S.; Ungar, A.R.; Lynch, K.R.
 Biochem. Biophys. Res. Commun. 279, 139-143, 2000
 A:Title: Characterization of a zebrafish (Danio rerio) sphingosine 1-phosphate receptor
 A:Reference number: J07559; MUID: 20563813; PMID:11112429
 A:Accession: J07559
 A:Molecule type: DNA
 A:Residues: 1-362 <IMA>
 A:Cross-references: GB:AF31294
 C:Comment: This receptor, a G protein-coupled receptor, mediates sphingosine 1-phosphate
 or also functions in the developing central nervous system in cell proliferation, apopto
 C:Genetics:
 A:Gene: edg1
 C:Superfamily: G protein-coupled receptor edg-1
 C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match	33.4%;	Score 656.5;	DB 2;	Length 362;
Best Local Similarity	41.0%;	Pred. NO. 1.9e-49;		
Matches 152;	Conservative 58;	Mismatches 136;	Indels 25;	Gaps 9;

[illegible]

RESULT 3

G protein-coupled receptor - human
C:Species: Homo sapiens (man)

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C:\Date: 13-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
C:\Accession: J05245
```

R; Yamaguchi, F.; Tokuda, M.; Hatase, O.; Brenner, S.

A/Title: Molecular cloning of the novel human G protein-coupled receptor (GPCR) gene map

A/Accession: JC5245
n/Reference number: 003243; MOLD:9/032811; PMID:88/8350

```
A;Molecule type: DNA
A;Residues: 1-378 <YAM>
```

A;C:Comment: This protein transduces hormone and neurotransmitter signals into A;C:Cross-references: EMBL:X838864; NID:g17703395; PIDN:CAA58744.1; PID:g17703396

C/Genetics:
A:Gene: $\alpha\alpha$ -3

A;Map position: 9q22.1-q22.2

C; keywords: G protein-coupled receptor

Query Match	32.8%;	Score 645.5;	DB 2;	Length 378;
Best Local Similarity	42.2%;	Pred. No. 1.8e-48;		
Matches 147;	Conservative 55;	Mismatches 133;	Indels 13;	Gaps 6

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0Y      28  HNHSGRGSLAGRGCPEDDGGALRGSLVSAOSCLVYENLVLAAITSNHRKRWYCYCLYN  87
      21  HGYVQKTLAIGRLKEASESTLTLYTELVICSEFYLENTLMVLAIWKNKPFNNRYFEIGN  80
0Y      88  IYLSOLLGAAYLAVLVLGSGARTFPLAPAOQMLERGLEFLTAALASTESLFTAGERATM  147
      81  LALCDLLAGIAIKVNIIMSGCKTBSLPTVYFIRGSGAFVALGASTCSLLAIAIERHLTM  140
0Y      148  VAPVAESGATKTSRYGFEIGCLMELALALGMIPLIGWNCICAFPGCSLPLYSKRYILF  207
      141  IK-MRPYDANKRHRVRELLIGMCMLIAFLTGLALPLIGWNCILNPDGSLPLYSKRYIAF  195
0Y      208  CLIVFAGVLATIMGLYGAIFRVLVOASGOKADRPARRKARRLKTVMILIAFLVCMGPL  267
      200  CISITFALTIVILYIARYIFLVKSSSKVANHNHNSERSMALTLRTVIVYVSFIACMSPL  259
0Y      268  FGLLIADYFGSLUWAQETLRCMDIMLAVLNSAVNPITYSKREYCAVLASTLCCGCL  327
      260  FILFLIDY-ACRVQACPLIFRAQOFIVYAVLNSAMNPVIYTLASKEMRAFFER-LVNCNL  317
0Y      328  RLGMGPGDCCLARAVEAHSGASTDSSLRPDRSGSLTSFRMRBPL  375
      318  ---VARGG---ARASPIOPALDPs---RSKSSSSNNSSHPKVEEDL  355
Db

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RESULT
A35300

G protein-coupled receptor edg-1 - human (Species: Homo sapiens (man))

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C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 24-Sep-1999
```

R; Hla, T.; Maciag,

A;Title: An abundant transcript ind

A;Accession: A35300
A;reference number: A35300; MUID:90284425; PMID:2100972

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A;Molecule type: mR
A;Residues: 1-381 <
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A;Cross-references: GB:M31210; NID:g181948; PIDN:AAA52336.1; PID:g181949
C:Genetics:

A; Gene: GDB:ECGF1

A;Map position: 22q13-22q13

Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane protein

Query Match 32.28; Score 633; DB 2; Length 381;

```

Best Local Similarity  40.5%;  Pred. NO. 2.2e-4/;
Matches 135;  Conservative 63;  Mismatches 125;  Indels 10;  Gaps 5;

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1 MNATGTPVAPESCOOTLAAGGHSRI.TVI.HYNHSGRI.AGGGPEPDGGI.GAI.BGI.SVAASCIY 60

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MCPTSVRIYKABSCSYDWNVDITVBNVNCTKI-NICADVENCTVIETCENIETTCOCT EO

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[illegible]

THESE ARE THE NAMES OF THE PERSONS WHO WERE
IN THE COUNTRY AT THE TIME OF THE RECENT
ATTACKS ON THE TOWNS OF BANGALORE AND MUMBAI.

121 REGLEFIALAASIFSLFIAGEKEAIMVRPVAESGATKITSRVGFGLCWLALALLGMLP 180

120 REGSMFVALSASVFSLAIAIERYITMLKMKLHNG-SNNFRLELLISACWVISLILGGLP 178

181 LLGWNCLCAFDRCSLLPLYSKRYILFCLVIFAGVLTIMGLYGAIFRLVQASGQKAPRP 240

b 179 IMGWNCISALSSCSTVLPYHKHYILECTVFTLLLSIVILYCRISLVRTSRRLTER 238

Y 241 AARRKARR-----LKTVMILLAFVWCWGPLEGLLADVFGSNLWAOEYLRGMDWILA 296

[illegible]

Db 239 KNISAKSRSENNALLKTYIIVLSVFIACAPLFIILLLDV-GCKVKTCIDILFRAEFLV 297

QY 295 LAVINSANVPITYSFRSREVCRAVLSFL-CCGC 326

Db 298 LAVLNGSTNPITITLTNKKEMRRAFIRIMSCCK 330

RESULT 5

JC1465

probable G protein-coupled receptor - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jul-2000

C:Accession: JC1465

C:Okazaki: H.; Ishizaka, N.; Sakurai, T.; Kurokawa, K.; Goto, K.; Kumada, M.; Takawa, Y. Biochem. Biophys. Res. Commun. 190, 1104-1109, 1993

A:Title: Molecular cloning of a novel putative G protein-coupled receptor expressed in th

A:Reference number: JC1465; MUID:93176155; PMID:8382486

A:Accession: JC1465

A:Molecule type: mRNA

A:Residues: 1-352 <OKA>

A:Cross-references: GB:AB016931; NID:g3445557; PIDN:BA32454.1; PID:g3445558

A:Experimental source: aortic smooth muscle

A:Superfamily: G protein-coupled receptor edg-1

C:Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane prot

F:67-95/Domain: transmembrane #status predicted <TM1>

F:110-128/Domain: transmembrane #status predicted <TM3>

F:148-173/Domain: transmembrane #status predicted <TM4>

F:190-210/Domain: transmembrane #status predicted <TM5>

F:234-255/Domain: transmembrane #status predicted <TM6>

F:272-293/Domain: transmembrane #status predicted <TM7>

F:13/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:142,145,218,219,329,330,331,332/Binding site: phosphate (Ser) (covalent) #status predi

F:313/Binding site: phosphate (Thr) (covalent) #status predicted

Query Match 26.3%; Score 517.5; DB 2; Length 352;

Best Local Similarity 38.4%; Pred. No. 2,3e-37;

Matches 127; Conservative 50; Mismatches 129; Indels 25; Gaps 7;

QY 10 PESCOQLAAGSHRLIVLHNHSGRLAGRGPEDEGLGALRGSLVAAACLVLENLLVLA 69

Db 11 PEKVOE-----HYNYTKETLDM-QETPSRKVASAFIILICCAIVENLLVLI 56

QY 70 AITSHMSRRMYVYCIYNITISDLTGAAVLANVLSGARFPRLAPAWOLFREGILFTAL 129

Db 57 AAVANSKFSHSMYFLGLAASDLAAGVAFVANTLISGPVTLSTPLQMFARREGSAFTTL 116

QY 130 AASTFSLFTAGEFPATVVRPAESGATKTSRYVGFITGLCWLIALALGLMPLLGWNCICA 189

Db 117 SASVFSLLAIAIEROVAIAK-VKLYGSDKSCRMMLIGASWLISLILIGLPIIGWNCIDH 175

QY 190 FDRCSLLPLYSKRYTILFCVIFPAGVLTATMGLGAIFRLVQASGOKAPPAARRKRRRL 249

Db 176 LEACSTVPLPYAKHYLCVVTIFSVILAIYALVIRYFVVRSSHADVAGP---QFLAL 231

QY 250 LKTYMILLATVCGMPLFGILLADVGSNMAOEYLRGMOWIILAVLNSAVNPITYSF 309

Db 232 LKTYVIVIGVFITLWLPFASITLDD-STCPYRACPVLYKAHYFAFATLSLNPVITYW 290

QY 310 RSREVCRAVLSFLC---GCLRLGMRG--PG 335

Db 291 RSRDLRRVLRPLLCWRGKATGRGNGPG 321

QY 310 RSREVCRAVLSFLC---GCLRLGMRG--PG 335

Db 291 RSRDLRRVLRPLLCWRGKATGRGNGPG 321

RESULT 6

JC5293

lysophosphatidic acid receptor - human

N:Alternate names: Edg2 protein

C:Species: Homo sapiens (man)

C:Date: 16-Apr-1997 #sequence_revision 09-May-1997 #text_change 10-Dec-1999

C:Accession: JC5293

R:An, S.; Dickens, M.A.; Bleu, T.; Hallmark, O.G.; Goetzl, E.J.

Biochem. Biophys. Res. Commun. 231, 619-622, 1997

A:Title: Molecular cloning of the human Edg2 protein and its identification as a func

A:Reference number: JC5293; MUID:97224397; PMID:9070858

A:Contents: Lung

A:Accession: JC5293

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-364 <ANA>

A:Cross-references: GB:U80811; NID:g1857424; PIDN:AAC51139.1; PID:g1857425

A:Superfamily: G protein-coupled receptor edg-1

Query Match 22.3%; Score 438; DB 2; Length 364;

Best Local Similarity 33.1%; Pred. No. 1.9e-30;

Matches 111; Conservative 54; Mismatches 152; Indels 18; Gaps 6;

QY 1 MNAITPAPPSCOQLAAG-----HSRLYLHNHSGR-LAGRGPEDEGLALRGISV 54

Db 1 MNAISTSPISVISOPEFTMANEPQCFYNSIAFFNRSKHLATMWNVS---KLYMGLGI 57

QY 55 AASCLVLENLLVLAITSNHSRRMYVYCIYNITISDLTGAAVLANVLSGARTERLA 114

Db 58 TYCITIMLANLVMVAIVNRRFHPPIYVLMANLAADFFAGLAFYLMFTGPNTRRLT 117

QY 115 PAQWFLREGILFTALASTFSLFTAGEFPATVVRPAESGATKTSRYVGFITGLCWLIA 174

Db 118 VSTWLLRGLIDTSLTASVANIATAIERHITFVRMQLHT-RMSNRVYVAVIWTWAI 176

QY 175 ILGMLPLIGWNCICAFDDCSSLLPLYSKRYTILFCVIFPAGVLTATMGLGAIFRLVQASG 234

Db 177 VNGALPDSGWNCTICDIENCSNAPISDSYLVFAIMLVFVYVAVYKAIHFGVQRRT 236

QY 235 OKAPPAARRKRR-----LKTVMILLAFVCGPLFGILLADVGSNMAOEYLRGM 289

Db 237 MMSMRSSSPRRNRDPMMSLKTIVYVIGAFITCWTGVLILDDVCCPQCDVLAVER-- 294

QY 290 DWILALVNSAVNPITYSFRSREVCRAVLSFLC 324

Db 295 FFLLLAEFNSAMNPITYSFRSREVCRAVLSFLC 328

QY 295 FFLLLAEFNSAMNPITYSFRSREVCRAVLSFLC 328

Db 295 FFLLLAEFNSAMNPITYSFRSREVCRAVLSFLC 328

RESULT 7

A33117

cannabinoid receptor CB1 - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 05-Nov-1999

C:Accession: A33117; C55879

R:Katsuda, I.A.; Lolait, S.J.; Brownstein, M.J.; Young, A.C.; Bonner, T.I.

Nature 346, 561-564, 1990

A:Title: Structure of a cannabinoid receptor and functional expression of the cloned

A:Reference number: A33117; MUID:90332039; PMID:2165569

A:Accession: A33117

A:Molecule type: mRNA

A:Residues: 1-473 <MAP>

A:Cross-references: GB:X55812; NID:g1552375; PIDN:CAA3932.1; PID:g57249

R:Shire, D.; Carillon, C.; Keshnd, M.; Calandra, B.; Rinaldi-carmona, M.; Le Fur, G.

J. Biol. Chem. 270, 3726-3731, 1995

A:Title: An amino-terminal variant of the central cannabinoid receptor resulting from

A:Reference number: A55879; MUID:95181329; PMID:7876112

A:Accession: C55879

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-107 <SHD>

C:Keywords: G protein-coupled receptor; glycoprotein; membrane protein

Query Match 17.9%; Score 351; DB 2; Length 473;

Best Local Similarity 30.1%; Pred. No. 9.1e-23;

Matches 105; Conservative 61; Mismatches 129; Indels 54; Gaps 11;

QY 48 ALRGLSVASCLVLENLLVLAITSNHSRRN-VYICLVNITISDLTGAAVLANVLL 105

Db 119 AIAVLSLTIGTFTVLEWLVLCVIL-HSRSLRCRPSYHIGSLAVADLGSVIFYVSFD 177

QY 106 SGARTFLAAGVFLRGLLFTLAASTFSLFTAGEFPATVVRPA-ESGATKTSRYVG 164

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Db      178 FHVHFRKSDPNVEFKRGVTA$F$TASVGSLEFLTAIDRI$T$H$RPLAYRI$VTR$P$A$V$A$ 237
QY      165 FTGLCWLALLIGMLP$LGWNC$LC$AFDRCS$LLP$Y$SKRY$ILF$CVI$F$AGV$LATI$MG$Y$G$ 224
Db      238 FC-LMWT$TAI$V$AV$P$LLG$MNC$K$LO$V$C$SDI$F$P$LI$DE$Y$LM$FWI$GV$SV$LL$F$LY$V$AM$ 296
QY      225 AIF-----RLVQASOKA-----PRPAR$R$AR$K$LT$V$M$ILL$A$F$V$C$ 263
Db      297 YILKMAH$H$A$V$H$A$V$DRG$T$OK$S$IT$HT$SE$D$K$V$O$V$TR$P$O$AR$M$D$I$LA$T$LV$IL$V$LV$IT$IC$ 356
QY      264 WGPLFGLLLADV$F$G$N$LM$A$O$E$Y$LR$G$M$W$IL-----AL$AV$N$A$V$P$II$Y$F$S$R$E$V$C$ 315
Db      357 WGPL$TAI$W$Y$D$V$E$K$-----M$N$K$LI$K$TV$F$A$F$C$M$LC$LN$ST$V$P$II$AL$S$K$D$IR$ 406
QY      316 RAVLSFL---CCGCLRL---GM$R$P$G$D$CL$AR$A$V$H$S$G$A$S$T$T$D$S$LR$P$R$D$S$ 360
Db      407 HAF$R$M$P$P$S$C$R$E$T$A$P$LD$N$S$K$G$D$S$CL-----N$H$N$A$N$T$S$M$H$R$A$E$S$ 449

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RESULT 8
E48909
G protein-coupled receptor Gprcrl3 - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 01-Dec-1995 #sequence_revision 01-Dec-1995 #text_change 19-May-2000
C:Accession: E48909
R:Wilkie, T.M.; Chen, Y.; Gilbert, D.J.; Moore, K.J.; Yu, L.; Simon, M.I.; Copeland, N.G.
Genomics 18, 175-184, 1993
A:title: Identification, chromosomal location, and genome organization of mammalian G-protein-coupled receptor Gprcrl3
A:Reference number: A48909; MUID:94116980; PMID:8288218
A:Accession: E48909
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-180 <WTL>
A:Cross-references: GB:J20334; NID:g438786; PIDN:AAA16846.1; PID:g438787
C:Superfamily: G protein-coupled receptor edg-1
C:Keywords: G protein-coupled receptor

Query Match	17.5%	Score 344.5	DB 2	Length 180
Best Local Similarity	43.58%	Pred. No. 1.2e-22		
Matches 77	Conservative 30	Mismatches 65	Indels 5	Gaps 2
QY	81	VYVYCLVNITLSDLLGAAVLAVNLGSGARTPLRPAQWFLREGLLFALAAASFISLLFRA	140	
DB	7	MYELGNLAASDLGAVAFVANTLTLGSHVITSLIPVQWFAREVSATFTLSASVSLIARA	66	
QY	141	GEFFATMPRPVASEGATTSRYGFTGLCWLIAALLGMPLELGNICADRCSSSLPLY	200	
DB	67	IEROVAALAK-VFLYGSDEKSCRMELMIGASMLITLIGLSITLGNCKNLKESATVLPYX	125	
QY	201	SKRYILFCFVIFAGVLATIMGIGYAFPLVQASQKAPRPARKAKARLLKTYLMLT	257	
DB	126	AKRYIVLCVTTISVLLAIVALKYIKFVAVSSHADVAG---QTALAKTYTIVL	178	

RESULT 9
S17595
cannabinoid receptor CBI - human
C:Species: Homo sapiens (man)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jul-2000
C:Accession: S17595; S13668; A55879
R:Gerard, C.M.; Mollereau, C.; Vassart, G.; Parmentier, M.
Biochem. J. 279, 129-134, 1991
A:Title: Molecular cloning of a human cannabinoid receptor which is also expressed in testis
A:Reference number: S17595; MUID:92028798; PMID:1718258
A:Accession: S17595
A:Molecule type: mRNA
A:Residues: 1-472 <GER1>
A:Cross-references: EMBL:X54937; NID:929914; PIDN:CAA8699.1; PID:q29915
R:Gerard, C.; Mollereau, C.; Vassart, G.; Parmentier, M.
Nucleic Acids Res. 18, 7142, 1990
A:Title: Nucleotide sequence of a human cannabinoid receptor cDNA.
A:Reference number: S13668; MUID:91088303; PMID:2263478
A:Accession: S13668

A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-472 <GER2>
A:Cross-references: EMBL:X54937; NID:g29914; PIDN:CAA3699.1; PID:g29915
R:Shire, D.; Caillion, C.; Kaghad, M.; Calandra, B.; Rinaud-Carmona, M.; Le Fur, G.,
J. Biol. Chem. 270, 3726-3731, 1995
A:Title: An amino-terminal variant of the central cannabinoid receptor resulting from
A:Reference number: A55879; MUID:95181329; PMID:7876112
A:Accession: A55879
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-124 <SH1>
A:Cross-references: CB:x81120
C:Genetics:
A:Gene: GDB:CNR1; CNR
A:Cross-references: GDB:127354; OMTM:114610
A:Map position: 6q14-6q15
C:Keywords: G protein-coupled receptor; glycoprotein; transmembrane protein
F:117-142/Domain: transmembrane #status predicted <TM>
F:155-115/Domain: transmembrane #status predicted <TM>
F:188-212/Domain: transmembrane #status predicted <TM>
F:233-256/Domain: transmembrane #status predicted <TM>
F:275-299/Domain: transmembrane #status predicted <TM>
F:345-365/Domain: transmembrane #status predicted <TM>
F:378-399/Domain: transmembrane #status predicted <TM>
F:777,83/Binding site: carboxylate (Asn) (covalent) #status predicted <TM7>

```

Query Match 15:99: Score 333: DB 21: Length 472:
Best Local Similarity 29.44: Pred. No. 3.3e-21:
Matches 105: Conservative 56: Mismatches 116: Indels 80: Gaps

QY 48 ALRLGSVAASCLVLENTLLVLAATTSNHRSSRR--VYCCLVNTPLSPDLLGAAYL----- 100
   :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 118 ALAVSLTGLGFYVLENTLVLCVLL-HSRSLRCRPSRHFGSLAVADLLSVTFVFSID 176
   :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :

QY 101 -----ANVLISGARTERLADPAQWFLREGLELTALASFTSLFTAGEREATVWRPV 151
   :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 177 FHVFRKRDNRVFL-----FKL-----GGVTASFASVGLFTLADRYTISHRPL 222
   :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :

QY 152 A-EGSARTKTSVYVFETIGCMTLLALGMLPLTGNCCLACDRSSLLPLYSKRIIFCLV 210
   :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 223 AYKRIIVRPKAVNAFC-LMMTIALIVAVLELLGNCKELQSVCSDFPHALDEYLFNFWIG 281
   :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :

QY 211 IFAGVLTATIMGLYGAIF-----RLVQASGOKA-----PREPARRRKARR 249
   :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 282 VTSVLLLEFIYAVAWYIIMKRAHSAVRKIQGTQKSIITHSEGGKVQVTRPDQARDIRL 341
   :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :

QY 250 LKIVYLLILLAEFLVCGWFLFGLLADYFGSMLMAQEYLRGMDWL-----ALAVNSA 301
   :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 342 AKTLVLLLVLLVLLICMGPILLAIWYDVCGK-----MNKLIKIVFAFCMSMLCNSGT 391
   :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :

QY 302 VNPIIVSFRRSEVCRANVLSFL--CCGGLRL--GMRRGPGCLAR-----AYEHSAGST 350
   :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 392 VNPIIVTASFDLEHARRSFPSCCEGTAPLDNSKSDSDILKHANNAAVSVHHAAES 448
   :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :

```

RESULT 10
A55689
G protein-coupled receptor 3 - human
N/Alternate names: G protein-coupled receptor GPR3; orphan G-protein-coupled receptor
C/Species: Homo sapiens (man)
C/Date: 03-Mar-1995 #sequence_revision 03-Mar-1995 #text_change 19-May-2000
C/Accession: A55689; S58521; C55733
R/Iismaa, T.P.; Kiefer, J.; Liu, M.L.; Baker, E.; Sutherland, G.R.; Shline, J.
Genomics 24, 391-394, 1994
A/Title: Isolation and chromosomal localization of a novel human G-protein-coupled re
A/Reference number: A55689; M0ID:95213036; PMID:7698767
A/Accession: A55689
A/Status: preliminary
A/Molecule type: DNA; mRNA
A/Residues: 1-330 <TTS>
A/Cross-references: GB:J32830; GB:J32831; NID:9602311; PIDN:AAA73560.1; PID:9602312
A/Berglückx, D.; Deneff, J.F.; Labbe, O.; Hayashi, Y.; Refetoff, S.; Vassart, G.; Parm

Biochem. J. 309, 837-843, 1995
A:Title: Molecular cloning of an orphan G-protein-coupled receptor that constitutively
A:Reference number: S58521; MUID:9536960; PMID:7639700
A:Accession: S58521
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-330 <EGG>
A:Cross-references: GB:X83956; NID:q1061125; PIDN:CAA58787.1; PID:q1061126
R:Marchese, A.; Docherty, J.M.; Nguyen, T.; Heiber, M.; Cheng, R.; Heng, H.H.Q.; Tsui, L.
Genomics 23, 609-618, 1994
A:Title: Cloning of human genes encoding novel G protein-coupled receptors.
A:Reference number: A5733; MUID:95154831; PMID:7851889
A:Accession: C55733
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-292 <MAR>
A:Cross-references: GB:U13668; NID:g577416; PIDN:AAA64594.1; PID:g577417
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 15.2%; Score 299.5; DB 2; Length 330;
Best Local Similarity 30.7%; Pred. No. 1.9e-18;
Matches 101; Conservative 49; Mismatches 138; Indels 41; Gaps 12;
QY 36 AGRG-----GPEGGGAGALRGLS-----VAASCVLENLVLAIATSHRSRR 79
DB 14 AAGSNVNSVGPAPGPAPAPLPSPKAMDVLCIGSTIVSCENLVAVIYGPAPFA 73
QY 80 WYTYCVNTTSDLTGAAYIANVLSCATFPRLAPQWFL-REGILFTALASTSLF 138
DB 74 PMFLVGLAVADLLAG---LGLVLFPAVFCIGSEMSLVGVVLAAMFTSISLLA 129
QY 139 TAGEFPATVWPVAESGATKTSRYVGFICMLLAILGMPLIGMNCICAFDRCSLLP 198
DB 130 ITVDRLTSLYNLTYSETVRYTYMALVWGALGLGLLPVLANNCIDGLTCCGVYP 189
QY 199 LYSKRIIFCLVTFAGVLTATMGLYATFRVY-----QASGQAPRPAPARRA-RRLKLT 252
DB 190 L-SKNLVLVLAIFPMVFGIMLOLYAQICRIVCHAAQOIALQRIPLPASTYVATRGKAT 248
QY 253 VLMTLAFVWGPFL-FGLLLADVFSGNLMAOEYLRGMDMLALAVNSAVNPITISFSS 311
DB 249 LAAVLGAFAACMLPFTVYCLGDASHPLYP--YL-----TLIPATYNSMINPIYAFRN 301
QY 312 REYCAVLSFLCCGC---LRLGMRGPD 336
DB 302 QDV-QKVLWAVCCSSSKIFPRSRPSD 329

RESULT 11

S40454
G protein-coupled receptor GPCR21 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 19-May-1994 #sequence_revision 10-Nov-1995 #text_change 20-Jun-2000
R:Accession: S40454
R:Saeki, Y.; Ueno, S.; Mizuno, R.; Nishimura, T.; Fujimura, H.; Nagai, Y.; Yanagihara, T.
FEBS Lett. 336, 317-322, 1993
A:Title: Molecular cloning of a novel putative G protein-coupled receptor (GPCR21) which
A:Reference number: S40454; MUID:94085630; PMID:8262253
A:Accession: S40454
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-330 <SAE>
A:Cross-references: GB:D21062; NID:9455487; PIDN:BA04641.1; PID:9455488
C:Superfamily: melanocortin receptor
C:Keywords: G protein-coupled receptor; phosphoprotein; transmembrane protein

Query Match 14.7%; Score 288.5; DB 2; Length 330;
Best Local Similarity 30.7%; Pred. No. 1.7e-17;

Matches 89; Conservative 51; Mismatches 125; Indels 25; Gaps 10;
QY 59 LVYLENLVLAITSMRSRRWYCYLVNTLSDLTGAAYIANVLSCATFRRL-APQA 117
DB 53 LVSCENLVAIVITGPAPAPAPFLVGSVAVADLLAG---LGLVLFPAADCCISPEM 108
QY 118 WFLREGILFTALASTFSLTFAGERFATVWPVAESGATKTSRYVGFICMLLAILG 177
DB 109 SLMLVGLVLAAPFASIGSLATTVDRYLSYNALTYSETVTFRTYMALVWVWGLG 168
QY 178 MFLGNCICAFDRCSLLPLYSKRIIFCLVTFAGVLTATMGLYATFRVY-----QA 232
DB 169 LVPVLAMNCRDGLTTCGVVYPL-SKNHLVLAIFEMVFGIMLOLYAQICRIVCHAAQOI 227
QY 233 SGQAPAPAPARRA-RRLKTYMLTILAFVWGPFL-FGLLLADVFSGNLMAOEYLRGMD 290
DB 228 ALQRHLLPASHYATKRGATLAVLVGFAPACWLPFTVYCLGDASHPLYP--YL----- 281
QY 291 WITLAVLNSAVNPITISFRRSREVCRAVLSFLCCGC---LRLGMRGPD 336
DB 282 -TLIPATYNSMINPIYAFRNQDV-QKVLMAICCCSTSKIFPRSRPSD 329

RESULT 12

S70364
cannabinoid receptor CB2, peripheral - mouse
N:Alternate names: G protein-coupled receptor CB2
C:Species: Mus musculus (house mouse)
C:Date: 21-Apr-1997 #sequence_revision 09-May-1997 #text_change 24-Sep-1999
R:Shire, D.; Calandra, B.; Rinaldi-Carmona, M.; Ousiric, D.; Pesssegue, B.; Bonnin-Cab.
Biochim. Biophys. Acta 1307, 132-136, 1996
A:Title: Molecular cloning, expression and function of the murine CB2 peripheral cann.
A:Reference number: S70364; MUID:96283604; PMID:8679654
A:Accession: S70364
A:Molecule type: mRNA
A:Residues: 1-347 <SHI>
A:Cross-references: EMBL:X86405; NID:g791081; PIDN:CAA60159.1; PID:g791082
C:Superfamily: melanocortin receptor
C:Keywords: G protein-coupled receptor; glycoprotein; transmembrane protein

Query Match 14.5%; Score 285; DB 2; Length 347;
Best Local Similarity 30.7%; Pred. No. 3.6e-17;
Matches 90; Conservative 45; Mismatches 108; Indels 50; Gaps 13;
QY 52 LSYAASC-----LVYLENLVLAITSMRSRRWYCYLVNTLSDLTGAAYIANVL 106
DB 34 IAAVLCITLMLGSLAENNAVLITLSRRLRRKSYLFIS-----SLAGADFLASYIF- 87
QY 107 GARTFRL-----APAQFLREGILFTALASTFSLTFAGERFATVWPVAESGATK 158
DB 88 -ACNFIHFVHFGVDNSNAIFLTKIGSVTWTFTASVGSLLTAVDRIYLCIPPYKALVY 146
QY 159 TSYRYGFIGC--WLLAAILGMPLIGMNCICAFDRCSLLP-----YSKRIIFCLVIF 212
DB 147 RGR--ALVALCWVWVLSALISYIPLMGWTC-CP-SPCELPFLPNDYLLGLMFLFIAL 202
QY 213 AGVLTATMGLYATF-----RLVQASGQAPAPAPARRARRLKLTVMITLAFVW 264
DB 203 SGITLYT---YGVVLMKARHVAETLAHEDROVPGIARMRLDVRLVLAIVLLICW 258
QY 265 GPLEGILLADVFSGNL---MAOEYLRGMDMLALAVLNSAVNPITISFRRSREV 314
DB 259 FPLALAM-----GHSIVTTLSDVKEAFVCSMLCLVNSAVNPITIALRSGEI 306

RESULT 13

S36750
cannabinoid receptor CB2 - human
N:Alternate names: cannabinoid receptor, peripheral
C:Species: Homo sapiens (man)
C:Date: 22-Jan-1994 #sequence_revision 10-Nov-1995 #text_change 17-Mar-1999
C:Accession: S36750

Mon Dec 9 12:35:25 2002

us-09-786-926-1.rpr

Page 7

Db 298 TFRKIIRSHVLR--RREPPKAGTISARALAAH-GSDGEQISLR 337

Search completed: December 9, 2002, 12:05:00
Job time : 22 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 9, 2002, 12:03:01 ; Search time 14 Seconds
(without alignments)
1137.636 Million cell updates/sec

Title: US-09-786-926-1

Perfect score: 1966
Sequence: 1 MNATGTPVAPBSCQOLAAG.....RSLSPRRRPLSSISVRSI 384

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	666	33.9	383	1	EDG1_RAT
2	645.5	32.8	378	1	EDG3_HUMAN
3	644	32.8	382	1	EDG1_MOUSE
4	633	32.2	381	1	EDG1_HUMAN
5	517.5	26.3	352	1	H218_RAT
6	444.5	22.6	364	1	EDG2_MOUSE
7	439	22.3	393	1	EDG2_SHEEP
8	438	22.3	364	1	EDG2_HUMAN
9	432.5	22.0	364	1	EDG2_BOVIN
10	351	17.9	473	1	CB1R_MOUSE
11	351	17.9	473	1	CB1R_RAT
12	346.5	17.6	470	1	CB1B_FURGU
13	345	17.5	472	1	CB1R_FELCA
14	344.5	17.5	180	1	EDG1_MOUSE
15	333	16.9	472	1	CB1R_HUMAN
16	330.5	16.8	473	1	CB1R_POEGU
17	330	16.8	468	1	CB1A_FURGU
18	317.5	16.1	473	1	CB1R_TARGR
19	299.5	15.2	330	1	GPR3_HUMAN
20	288.5	14.7	330	1	GPR3_MOUSE
21	285	14.5	347	1	CB2R_MOUSE
22	285	14.5	360	1	CB2R_RAT
23	281.5	14.3	360	1	CB2R_HUMAN
24	258.5	13.1	334	1	GP12_HUMAN
25	256.5	13.0	334	1	GP12_MOUSE
26	256.5	13.0	334	1	GP12_RAT
27	248.5	12.6	362	1	GPR6_HUMAN
28	248.5	12.6	412	1	AA2A_CANFA
29	245	12.5	363	1	GPB6_RAT
30	244.5	12.4	412	1	AA2A_HUMAN
31	236.5	12.0	325	1	MC5R_HUMAN
32	235	12.0	361	1	OPSB_CHICK
33	234.5	11.9	325	1	MC5R_PANTR

34	233.5	11.9	410	1	AA2A_RAT	P30543	rattus norv
35	231.5	11.8	561	1	ALAD_RAT	P23944	rattus norv
36	230	11.7	402	1	OPN3_HUMAN	Q9H1Y3	homo sapien
37	230	11.7	410	1	AA2A_MOUSE	Q60613	mus musculu
38	228.5	11.6	409	1	AA2A_CAVPO	P46616	cavia porce
39	228	11.6	572	1	ALAD_HUMAN	P25100	homo sapien
40	227.5	11.6	348	1	ALAD_HUMAN	O62798	tursiops tr
41	227.5	11.6	355	1	OPSD_TURFA	P51472	astyanax fa
42	227.5	11.6	388	1	5H4_CAVPO	O70528	cavia porce
43	224.5	11.4	388	1	5H4_MOUSE	P97288	mus musculu
44	223	11.3	576	1	ALAD_RABIT	O02666	oryctolagus
45	222	11.3	314	1	MSHR_CHICK	P55167	gallus galli

ALIGNMENTS

```

RESULT 1
EDG1_RAT
ID
AC P48303; STANDARD; PRT; 383 AA.
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Probable G protein-coupled receptor EDG-1.
GN EDG1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Cerebellum;
RX MEDLINE=95047496; PubMed=7959012;
RA Lado D.C., Browe C.S., Gaskin A.A., Borden J.M., MacLennan A.J.;
RT "Cloning of the rat edg-1 immediate-early gene: expression pattern
RT suggests diverse functions.";
RL Gene 149:331-336 (1994).
CC -!- FUNCTION: IT IS POSSIBLE THAT IT ACTS AS A RECEPTOR FOR A TROPHIC
CC FACTOR AND IS INVOLVED IN THE SURVIVAL OF BRAIN CELLS.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- DEVELOPMENTAL STAGE: FIRST DETECTED AT EMBRYONIC DAY 15. AT
CC POSTNATAL DAY 14 DETECTED IN SKIN, SPLEEN, LIVER, KIDNEY, HEART,
CC TESTICLE, LUNG AND BRAIN. AT ADULTHOOD IS MOST ABUNDANT IN BRAIN.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U10303; AA83418.1; -
CC InterPro: IPR002761; GPCR_Rhodpsn.
CC InterPro: IPR004061; S1Receptor.
CC Pfam: PF00001; 7tm.1; 1.
CC PRINTS; PR00237; GPCR_RHODPSN.
CC PRINTS; PR01523; S1RECEPTOR.
CC PROSITE; PS00237; G-PROTEIN_RECPT-FL_1; 1.
CC PROSITE; PS0262; G-PROTEIN_RECPT-FL_2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein;
CC Phosphorylation; Lipoprotein; Palmitate.
CC DOMAIN 1 47
CC TRANSMM 48 72 EXTRACELLULAR (POTENTIAL).
CC DOMAIN 73 79 CYTOPLASMIC (POTENTIAL).
CC TRANSMM 80 108 2 (POTENTIAL).
CC DOMAIN 109 122 EXTRACELLULAR (POTENTIAL).
CC TRANSMM 123 141 3 (POTENTIAL).
CC DOMAIN 142 160 CYTOPLASMIC (POTENTIAL).
CC TRANSMM 161 186 4 (POTENTIAL).
CC DOMAIN 187 202 EXTRACELLULAR (POTENTIAL).

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FT TRANSMEM 203 223 5 (POTENTIAL).
FT DOMAIN 224 257 6 (POTENTIAL).
FT TRANSMEM 258 279 6 (POTENTIAL).
FT DOMAIN 280 295 6 (POTENTIAL).
FT TRANSMEM 296 316 7 (POTENTIAL).
FT DOMAIN 317 383 7 (POTENTIAL).
FT CARBOHYD 31 31 7 (POTENTIAL).
FT LIPID 329 329 7 (POTENTIAL).
FT MOD.RES 354 354 7 (POTENTIAL).
SQ SEQUENCE 383 AA: 42745 MW: 090BAAE09D4F3 CRC64:

Query Match 33.9%; Score 666; DB 1; Length 383;
Best Local Similarity 40.0%; Pred. No. 2.1e-37;
Matches 150; Conservative 69; Mismatches 126; Indels 30; Gaps 8;

OY 1 MNATGPVAPESQOQLAAGHSRLVLAHNSHGRGKRGPDGGLGALRGISVASCIV 60
DB 2 VSTSLIPVVKALRSQVSDGNDIVRHNYNKGKL-NIGVEKDHGIKLTSVFILICLI 60
OY 61 VLENLVLVAITSHMSRRMYVYCVNITLSDLTGAAYLANVLGARTFPLAPOMFL 120
DB 61 ILENFVLLTIKTKKHFHMPYFIGNLALSDLLAGVATYANLISGATTKLPAPOMFL 120
OY 121 REGCLFTALASTFSLFTAGGERFATWVPAESGATTSRYGFIQCLWLLALGLMP 180
DB 121 RGSMEVALASVFSILAIERITMLKMLHNG-SNSSRFLISACWYISLIGLPL 179
OY 181 LIGMNCIAFDRCSLLPLYSKRYTLFCLVIFAGVLAITIMLGKIFLVAQSGO----- 235
DB 180 IGMWNCISLSCSTVLPYKHNYLFTCTVFTLLLSIVLICYISLVTRSRRLTFR 239
OY 236 ---KAPRPARRRARLLKTVLMLLAFVCMGPFLLADVFGSMLMAOEYLRGMW 291
DB 240 KNISKASR--SSEKISALLKTYIIVLSVFIACWAPLFLILLDV-GCAKAKCDILYKREY 296
OY 292 ILALVMSAVNPITYSRSREVCNAVLSFL-CCGCLFLKMG-----PGDCLARAVE 343
DB 297 FLVLAVLNSGTPILTYLTINEMRAFLRIISCCPCNGSAGKFKRPILIPMEFSR--- 353
OY 344 AHSGASTTDSLRPR 358
DB 354 -----SKSDNSHPQ 363

RESULT 2
EDG3_HUMAN STANDARD: PRT: 378 AA.
ID EDG3_HUMAN Q99500:
AC Q99500:
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Lysosphingolipid receptor (EDG-3).
GN EDG3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
CC NCBI_TaxID=9606;
RX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=97032811; PubMed=8878560;
RA Yamaguchi F., Tokuda M., Hatase O., Brenner S.;
RT "Molecular cloning of the novel human G protein-coupled receptor
RT (GPCR) gene mapped on chromosome 9.";
RL Biochem. Biophys. Res. Commun. 227:608-614(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=98072391; PubMed=9409733;
RA An S., Bleu T., Huang W., Hallmark O.G., Coughlin S.R., Goetzl E.J.;
RT "Identification of cDNAs encoding two G protein-coupled receptors for
RT lysosphingolipids.";
RL FEBS Lett. 417:279-282(1997).

```

```

CC -1- FUNCTION: ORPHAN RECEPTOR.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN ALL TISSUES, BUT MOST ABUNDANTLY
CC IN HEART, PLACENTA, KIDNEY, AND LIVER.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----
DR EMBL: X83864; CA58744.1; -.
DR EMBL: AF022139; AAC51906.1; -.
DR Genew: HGNC:3167; EDG3.
DR MIM: 601965; -.
DR InterPro: IPR004062; EDG3receptor.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR01524; EDG3RECEPTOR.
DR PRINTS: PR00237; GPCRHHODOPS.
DR PRINTS: PR01523; S1PRECEPTOR.
DR PROSITE: PS00237; G_PROTEIN_RECPT_F1_1; 1.
DR PROSITE: PS0262; G_PROTEIN_RECPT_F1_2; 1.
DR G-protein coupled receptor; Transmembrane; Glycoprotein.
KW DOMAIN 1 40
FT TRANSMEM 41 65
FT DOMAIN 66 72
FT TRANSMEM 73 101
FT DOMAIN 102 115
FT TRANSMEM 116 134
FT DOMAIN 135 153
FT TRANSMEM 154 179
FT DOMAIN 180 195
FT TRANSMEM 196 216
FT DOMAIN 217 243
FT TRANSMEM 244 265
FT DOMAIN 266 281
FT TRANSMEM 282 302
FT DOMAIN 303 378
FT CARBOHYD 15 15
SQ SEQUENCE 378 AA: 42294 MW: 79A00306203F439F CRC64:

Query Match 32.8%; Score 645.5; DB 1; Length 378;
Best Local Similarity 42.2%; Pred. No. 4.8e-36;
Matches 147; Conservative 55; Mismatches 133; Indels 13; Gaps 6;

OY 28 HYNHSGRLRGSGPDEGGGALRGISVASCIVLENLVLVAITSHMSRRMYVYCVN 87
DB 21 HYIYVKLGRLEKASEGSTLTITVLEFLVICSFTVLENLWVLAIAIKNNKFNRMTEFGN 80
OY 88 ITLSDLLTGAAYLANVLGARTFPLAPOMFLREGILFTALASTFSLFTAGGERFATM 147
DB 81 LALCDLLAGIAVKVNTLMGSKTFFSLPTVWFLRSGSMKVALGASTCLALAIIRHLTM 140
OY 148 VRPVASGATKTSRYVGFGLCWLAALLGMLPLIGMNCIAFDRCSLLPLYSRYTLF 207
DB 141 IK-MRPYDANKRRHREFLLIGMCMIAFTGLALPIIGMNCIHLNIPDCSTILPLSKRYIAF 199
OY 208 CVIYFAGVLAITMGVYGFRLVVOASGOKAPRPARRRARLLKTVLMLLAFVCMG 267
DB 200 CISIFAILVTIYILKARYIFLYKSSSRKVVAHNNNSRMALRTVIVVSVFIACWSP 259
OY 268 FGLLADVFGSMLMAOEYLRGMWTLALAVLSAVNPITYSRSREVCNAVLSFLCCGCL 327
DB 260 FILFLIDV-ACRVQACPLIFKAQWFLVAVLSANNPIYITLASEMRRAFFR-LVNCNL 317
OY 328 RLGMSGPGCLARAVAHSGASTTDSLRPRDSFGSGLSRMRKPL 375
DB 318 ---VGRG---ARASPIOPALDPS-----RSKSSSSNNSSHSPKVEDL 355

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RESULT 3	EDGL_MOUSE	STANDARD:	PRT:	382 AA.
ID	EDGL_MOUSE			
DN	01-NOV-1997 (Rel. 35, Created)			
DN	01-NOV-1997 (Rel. 35, Last sequence update)			
DN	15-JUL-1998 (Rel. 36, Last annotation update)			
DE	Probable G protein-coupled receptor EDG-1.			
GN	EDG1.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_Taxid=10090;			
RP	[1]			
RC	SEQUENCE FROM N.A.			
RC	SPRAIN-BALB/C; TISSUE=Liver;			
RX	MEDLINE=97369927; PubMed=9226368;			
RA	Liu C.H., Hla T.;			
RT	"The mouse gene for the inducible G-protein-coupled receptor edg-1.";			
RL	Genomics 43:15-24(1997).			
CC	-1- FUNCTION: THIS INDUCIBLE EPITHELIAL CELL G-PROTEIN-COUPLED RECEPTOR MAY BE INVOLVED IN THE PROCESSES THAT REGULATE THE DIFFERENTIATION OF ENDOTHELIAL CELLS (BY SIMILARITY).			
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.			
CC	-1- TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES WITH HIGHEST LEVELS IN BRAIN, SPLEEN AND HEART. LOWER LEVELS FOUND IN LUNG, PLACENTA, MUSCLE, LIVER, UTERUS AND KIDNEY. VERY LOW LEVELS IN TESTIS AND THYMUS.			
CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.			
CC	-----			
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CC	-----			
DR	EMBL; U40811; AAC53294.1; -.			
DR	MDJ; MG1:1096355; Edg1.			
DR	Interpro; IPR000276; GPCR_Rhodopsn.			
DR	Interpro; IPR004061; SlpReceptor.			
DR	Pfam; PF00001; 7tm_1.1.			
DR	PRINTS; PR00237; GPCRHHODPSN.			
DR	PRINTS; PR01523; SlpRECEPTOR.			
DR	PROSITE; PS00237; G-PROTEIN_RECPT_FL1.1; 1.			
DR	PROSITE; PS50262; G-PROTEIN_RECPT_FL2.1.			
KW	G-protein coupled receptor; Transmembrane; Glycoprotein;			
KW	Phosphorylation; Lipoprotein; Palmitate.			
FT	DOMAIN	1	46	EXTRACELLULAR (POTENTIAL).
FT	DOMAIN	47	71	1 (POTENTIAL).
FT	DOMAIN	72	78	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	79	107	2 (POTENTIAL).
FT	DOMAIN	108	121	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	122	140	3 (POTENTIAL).
FT	DOMAIN	141	159	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	160	185	4 (POTENTIAL).
FT	DOMAIN	186	201	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	202	222	5 (POTENTIAL).
FT	DOMAIN	223	256	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	257	278	6 (POTENTIAL).
FT	DOMAIN	279	294	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	295	315	7 (POTENTIAL).
FT	DOMAIN	316	382	CYTOPLASMIC (POTENTIAL).
FT	CARBOHYD	30	30	GLYCOSYLATION (POTENTIAL).
FT	LIPID	328	328	NON-LINKED (BY SIMILARITY).
FT	MOD. RES	353	353	PHOSPHORYLATION (POTENTIAL).
SO	SEQUENCE	382 AA;	42571 MW;	A004693491C8957 CRC64;
Query Match		32.8%;	Score 644;	DB 1; Length 382;
Best Local Similarity		38.9%;	Pred. NO. 6.1e-36;	

```

Matches 1; Conservative 67; Mismatches 135; Indels 26; Gaps 7;
OY 1 MNACGTVAEESCOOLACAGHSRLIVAHYHNSGRLAGCGPEDGCLALGSLVMAASCV 60
DB 1 MVSTSIPEVKALSSVSDYGDNDIYRHNVTGKL-NIGAEKDGKILSVTFLLCCET 59
OY 61 VLENLVLAAITSHMSRRMYVYCLVNTITLSDLTGAAYLANVLLSGARTFRLAPAWML 120
DB 60 ILENIPLLTIMTKKFRHMYEFIGNLALSDCLAGVATYANLLSGATYTKLTPAWML 119
OY 121 REGLLPALASRFSLLTFAGERFATMPVPAVESGATGTSRYVGIGLMLLAALGMLP 180
DB 120 REGSMFALASVFSLLATAIERYITLMKMKHNG-SNSSFLLISACAVIILGGLP 178
OY 181 LIGMNCICADRSSLLPLYSKRYITFCVLVPAGVATIMGLYCATIRLYQASGK- 236
DB 179 SMGNMNCISSISVLPYTHKRYITFCVTYPTLLSIALYCRISLYLRTSRRTFR 238
OY 237 --APRPAARRKARKRLKTVLMLLAFLVCMGPLEGILLADVFSGNLMAOYELRGMDWIL 293
DB 239 KNISGRSSSEKSLAKLTQVITVLSVFICMAPLEFILLLLDV-GCKAKTODIYKAEYFL 297
OY 294 ALAVLNAVVPYIYPSRFEVCAYVSFL-CCGCCIRLGMRG-----PPDCIARVAEAH 345
DB 298 VLAIVLNSGTPIIYITLNKEMRAFRIRYSCCKCPGNSAKCFKFRPIIPGMEFSR----- 352
OY 346 SGASTDSSLRPR 358
DB 353 --SKSDNSSHPQ 362

RESULT 4
EDGL_HUMAN
ID EDGL_HUMAN STANDARD; PRT; 381 AA.
AC P21453;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Probable G protein-coupled receptor EDG-1.
GN EDGL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
CX NCBI_Taxid:9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=umbilical vein endothelial cells;
RX MEDLINE=90264425; Pubmed=2160972;
FA Hla 1., Macgill T.;
RT "An abundant transcript induced in differentiating human endothelial
RT cells encodes a polypeptide with structural similarities to
RT G-protein-coupled receptors."
RL J. Biol. Chem. 265:9308-9313(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=98072391; Pubmed=9409733;
RA An S., Bieu T., Huang W., Hallmark O.G., Coughlin S.R., Geetzl E.J.;
RT "Identification of cDNAs encoding two G protein-coupled receptors for
RT lysophingolipids."
RL FEBS Lett. 417:279-282(1997).
RN [3]
RP FUNCTION: THIS INDUCIBLE EPITHELIAL CELL G-PROTEIN-COUPLED
RP RECEPTOR MAY BE INVOLVED IN THE PROCESSES THAT REGULATE THE
RP DIFFERENTIATION OF ENDOTHELIAL CELLS.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: ENDOTHELIAL CELLS, AND TO A LESSER EXTENT, IN
CC VASCULAR SMOOTH MUSCLE CELLS, FIBROBLASTS, MELANOCYTES, AND CELLS
CC OF EPITHELIOID ORIGIN.
CC -1- INDUCTION: BY THE TUMOR PROMOTER PHORBOL 12-MYRISTATE 13-ACETATE
CC (PMA) IN THE PRESENCE OF CYCLOHEXIMIDE.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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DR EMBL: M31210; AAA52336.1; -
 DR EMBL: AF022137; AAC51905.1; -
 DR PIR: A35300; A35300.
 DR Genew: HGNC:3165; EDG1.
 DR MIM: 601974; -
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR InterPro: IPR004061; S1preceptor.
 DR Pfam: PF00001; 7tm.1; 1.
 DR PRINTS: PR000237; GPCR_RHODOPSN.
 DR PRINTS: PR01523; S1PRECEPTOR.
 DR PROSITE: PS00237; G_PROTEIN_RECPT_F1_1; 1.
 DR PROSITE: PS00262; G_PROTEIN_RECPT_F1_2; 1.
 DR G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW Phosphorylation; Lipoprotein; Palmitate.
 FT DOMAIN 1 46
 FT TRANSMEM 47 71
 FT DOMAIN 72 78
 FT TRANSMEM 79 107
 FT DOMAIN 108 121
 FT TRANSMEM 122 140
 FT DOMAIN 141 159
 FT TRANSMEM 160 185
 FT DOMAIN 186 201
 FT TRANSMEM 202 222
 FT DOMAIN 223 255
 FT TRANSMEM 256 277
 FT DOMAIN 278 293
 FT TRANSMEM 294 314
 FT DOMAIN 315 381
 FT CARBOHYD 30 30
 FT CARBOHYD 36 36
 FT LIPID 327 327
 FT MOD_RES 352 352
 FT SEQUENCE 381 AA; 42695 MW; D706DA4C74C2E093 CRC64;

Query Match 32.2%; Score 633; DB 1; Length 381;
 Best Local Similarity 40.5%; Pred. NO. 3.2e-35;
 Matches 135; Conservative 63; Mismatches 123; Indels 10; Gaps 5;

QY 1 MNAETPVAPESQQLAAGSHRLIVLYNHSGLAARGGPDGGLGALGLSVAAACLV 60
 DB 1 MGPTSPVLKARHSSVDVNDIVRYNTGKL-NISADKENSILKTSVFLICPFI 59
 QY 61 VLENLVLVAITSHMSRMVYVCVNTTSLDLTGAAYLANVLSGARFRLAPQWFL 120
 DB 60 ILENIVLLTIWTKKFFHFMPTFFIGNALSLDLAAGVAYRANLLISATTYKLTLPQWFL 119
 QY 121 REGLEFALAASTFSLTAGRFRATVVRPAVESGARFTRSYVYGLCMLLAALGLMP 180
 DB 120 REGSMFVALASAVSFSLAIAIRYITMKMLHNG-SNNEFLFLISACVWISLIIGDP 178
 QY 181 ILGMNCAAFDRCSLLPLYSKRYTLFCLVFAVLATIMGLGALIPRLVOAGSKAPP 240
 DB 179 IMGNMCAISLSCSYLPLRYHKHYTLFCTYVFTLLISLYIKRISYVTRTSRRLTR 238
 QY 241 AARRKARR-----LKYVLMMLLFLVCGPPLFGLLADVFSGNMAOQYLRGMWILA 294
 DB 239 KNISKSRSENVALLKTYIIVLSVFIACMAPLFTLLLLDV-GCKVYTCIDILFRAYFLV 297
 QY 295 LAVLNAVNPITISFRSRECAVLSFL-CCGC 326
 DB 298 LAVLNGSTNPITITLLNKEMRAFLRIMSCCKC 330

RESULT 5
 H218_RAT

ID H218_RAT STANDARD: PRT: 352 AA.
 AC P47752;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Probable G protein-coupled receptor H218 (AGRI6) (lysosphingolipid
 DE receptor).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain, and Lung;
 RX MEDLINE=94373324; PubMed=8087418;
 RA MacLennan A.J., Browe C.S., Gaskin A.A., Lado D.C., Shaw G.;
 RT "Cloning and characterization of a putative G-protein coupled
 RT receptor potentially involved in development."; Mol. Cell. Neurosci. 5:201-209(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=ortic smooth muscle;
 RX MEDLINE=93176155; PubMed=8382486;
 RA Okazaki H., Ishizaka N., Sakurai T., Kurokawa K., Goto K.,
 RT "Molecular cloning of a novel putative G protein-coupled receptor
 RT expressed in the cardiovascular system."; Biochem. Biophys. Res. Commun. 190:1104-1109(1993).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=98072991; PubMed=9409733;
 RA An S., Blau T., Huang W., Hallmark O.G., Coughlin S.R., Goetzl E.J.;
 RT "Identification of cDNAs encoding two G protein-coupled receptors for
 RT lysophingolipids."; FEBS Lett. 417:279-282(1997).
 RL
 CC -1- FUNCTION: POSSIBLE RECEPTOR FOR THE LYSPHINGOLIPIDS SPHINGOSINE
 CC -1- PHOSPHATE (SLP) AND DIHYDRO-SLP.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL IN ALL DEVELOPING TISSUES WITH
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN PRIMITIVE, TRANSFORMED CELLS. RELATIVE
 CC HIGHEST LEVELS DETECTED IN PRIMITIVE, TRANSFORMED CELLS. RELATIVE
 CC ABUNDANCE: LUNG > KIDNEY = SKIN = GUT > SPLEEN > BRAIN > LIVER.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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FT DOMAIN 174 189 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 190 210 5 (POTENTIAL).
FT DOMAIN 211 233 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 234 253 6 (POTENTIAL).
FT DOMAIN 256 271 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 272 292 7 (POTENTIAL).
FT DOMAIN 293 352 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 19 19 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT LIPID 305 305 PALMITATE (BY SIMILARITY).
SQ SEQUENCE 352 AA; 38734 MW; 9C933A18E756CE1E CRC64;

Query Match 26.3%; Score 517.5; DB 1; Length 352;
Best Local Similarity 38.4%; Pred. No. 1.3e-27;
Matches 127; Conservative 50; Mismatches 129; Indels 25; Gaps 7;

QY 10 PESCOQLAAGHSHRLIVLHYNHSGRLAGRGEPEDGGLALGRLSYAASCLVLENLVLVA 69
DB 11 PEKVOE-----HNYTKETLDM--QETPSRKVASAFITILCAIYVENLVLVI 56
QY 70 AITSHMRKRWYVYCLVNTITSLDITGAAYLANVLLSGARFRLAPAGMFLREGILFTAL 129
DB 57 AARNSKFSHSAHYLFLGNLAASDLAAGAAEVANLTLGSPVTLSTPLQWFAREGSAFTTL 116
QY 130 AASTSLFTAGEFRATVWRPVAESGATRTSRVYFGTGLMALLGLMPLLGWNCICA 189
DB 117 SASVSLAIALEROVAIK-VKLYGSDKSCMLMIGASMLISLILGPILGWNCIDH 175
QY 190 FDRGSSLLPLYSKRYTFLCLVTFAGVATIMGLYAIFFLVOASGOKAPRPAARRARRL 249
DB 176 LEAGSTVLPYAKHYVLCVTFESVYLLALVALYRIFVYVSSHADVAGP---QTLAL 231
QY 250 LRTVIMLILAFVCGPLFGILLADVFSGNLMAQETLRMBMILLAVLNSAVNNTIYSF 309
DB 232 LKTVITLVGVFLICMLPASITLED-STCPVACPVLYKAHFAPATLNSLNPVIYTW 290
QY 310 RSREVCRAVLSFLCC---GCLRGLMRG--PG 335
DB 291 RSRDLREVLRLPLCMRGKATGRRGNPG 321

RESULT 6
EDG2 MOUSE STANDARD: PRT: 364 AA.
ID EDG2 MOUSE
AC 061130; P70420; P56487;
DT 01-NOV-1997 (Rel. 35; Created)
DT 15-JUL-1998 (Rel. 36; Last sequence update)
DE 16-OCT-2001 (Rel. 40; Last annotation update)
DE Lysophosphatidic acid receptor (EDG-2) (RECL.3) (VZG-1).
GN EDG2 OR GPCR26 OR VZG1.
OS Mus musculus (Mouse) and
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090, 10116;
RN 11
RP SEQUENCE FROM N.A.
RC SPECIES=Mouse; STRAIN=BALB/c;
RA MEDLINE=97081105; PubMed=8922387;
RA Hecht J.H., Weiner J.A., Post S.R., Chun J.;
RT "Ventricular zone gene-1 (vzg-1) encodes a lysophosphatidic acid
RT receptor expressed in neurogenic regions of the developing cerebral
RT cortex";
RL J. Cell Biol. 135:1071-1083(1996).
RN 12
RP SEQUENCE OF 19-364 FROM N.A.
RC SPECIES=Mouse; STRAIN=C57BL/6; TISSUE=Brain;
RA MEDLINE=97165887; PubMed=9013780;
RA MacIre A.D., Premont R.T., Jaber M., Petersen A.S., Leikowitz R.J.;
RT "Cloning, characterization, and chromosomal localization of recl.3, a
RT member of the G-protein-coupled receptor family highly expressed in
RT brain.";
RL Brain Res. Mol. Brain Res. 42:245-254(1996).
RN 13
```

```
RP SEQUENCE FROM N.A.
RC SPECIES=Rat; STRAIN=Sprague-Dawley; TISSUE=Olfactory bulb;
RA MEDLINE=98424094; PubMed=9753172;
RA Allard J., Barron S., Diaz J., Lubetzki C., Zalc B., Schwartz J.-C.,
RA Sokoloff P.;
RT "A rat G protein-coupled receptor selectively expressed in myelin-
RT forming cells.";
RL Eur. J. Neurosci. 10:1045-1053(1998).
CC -1- FUNCTION: RECEPTOR FOR LYOPHOSPHATIDIC ACID (LPA), A MEDIATOR OF
CC DIVERSE CELLULAR ACTIVITIES.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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CC EMBL: U70622; AAC52923.1; -

CC EMBL: U48235; AAC53035.1; -

CC EMBL: AF014418; AAB86381.1; -

CC MGI: 108429; Edg2.

CC InterPro: IPR000276; GPCR_Rhodpsn.

CC InterPro: IPR004065; LPAREceptor.

CC Pfam: PF00001; 7tm_1; 1.

CC PRINTS: PRO1527; LPARECEPTOR.

CC PROSITE: PS00237; G-PROTEIN_RECPT_P1_1; 1.

CC PROSITE: PS0262; G-PROTEIN_RECPT_P1_2; 1.

CC G-protein coupled receptor; Transmembrane; Glycoprotein;

CC Phosphorylation; Lipoprotein; Palmitate.

CC DOMAIN 1 50 EXTRACELLULAR (POTENTIAL).

CC DOMAIN 1 75 1 (POTENTIAL).

CC DOMAIN 76 82 CYTOPLASMIC (POTENTIAL).

CC DOMAIN 83 111 2 (POTENTIAL).

CC DOMAIN 112 125 EXTRACELLULAR (POTENTIAL).

CC DOMAIN 126 144 3 (POTENTIAL).

CC DOMAIN 145 163 CYTOPLASMIC (POTENTIAL).

CC DOMAIN 164 189 4 (POTENTIAL).

CC DOMAIN 190 205 EXTRACELLULAR (POTENTIAL).

CC DOMAIN 206 226 5 (POTENTIAL).

CC DOMAIN 227 258 CYTOPLASMIC (POTENTIAL).

CC TRANSMEM 259 280 6 (POTENTIAL).

CC TRANSMEM 281 294 EXTRACELLULAR (POTENTIAL).

CC DOMAIN 295 315 7 (POTENTIAL).

CC TRANSMEM 316 364 CYTOPLASMIC (POTENTIAL).

CC DOMAIN 327 327 PALMITATE (BY SIMILARITY).

CC LIPID 27 27 N-LINKED (GLCNAC. . .) (POTENTIAL).

CC CARBOHYD 35 35 N-LINKED (GLCNAC. . .) (POTENTIAL).

CC CONFLICT 225 225 Y -> S (IN REF. 2).

CC SEQUENCE 364 AA; 41119 MW; B0FA6265AA68857 CRC64;

Query Match 22.6%; Score 444.5; DB 1; Length 364;

Best Local Similarity 34.3%; Pred. No. 8.6e-23;

Matches 106; Conservative 51; Mismatches 141; Indels 11; Gaps 4;

QY 21 HSRLLVHYNHSGRLAGRGEPEDGGLALGRLSYAASCLVLENLVLVAATTSMRBRW 80

DB 26 YNESIAFFYNRSGKYLATEWNTVSKL--VMGLITVCVFIMLNLVLAIVYVNRHFP 83

QY 81 VYCCVNTITSLDITGAAYLANVLLSGARFRLAPAGMFLREGILFTALASTSLFETA 140

DB 84 IYTLMANLAADFRAGLAFYFLMFGTGNTRKRLVSTMLDGLIDSLTASVANLLAIA 143

QY 141 GERFATVWRPVAESGATRTSRVYFGTGLMALLGLMPLLGWNCICAFDRCSLLPLY 200

DB 144 IERHITVFRMQLHT-RMSNRRVYVYIYIMTAIYGAIPSGWNCICDDIDHCSNMAPLY 202

QY 201 SKRYTLFCLVTFAGVATIMGLYAIFFLVOASGOKAPRPAARRARRR-----LLKTVIM 255

DB 203 SDSYLVFAIFNLVTFVYVAVVLYAHIFGYVRQRTMRSSSGPRRSDTMMSLKTVI 262

SEQUENCE	AA;	44433 MW;	356E961153C345FC CRC64;
393	AA;	44433 MW;	356E961153C345FC CRC64;

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CC or send an email to license@lsb-sib.ch.
CC -----

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DR EMBL: U08011; AAC51139.1; -
DR EMBL: Y09479; CAAT0686.1; -
DR EMBL: Y09479; CAAT0687.1; -
DR EMBL: U78192; AAC00530.1; -
DR Genew: HGNC:3166; EDG2.
DR MIM: 602282; -
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR InterPro: IPR004065; LPareceptor.
DR Pfam: PF00001; 7tm.1; 1.
DR PRINTS: PR01527; LPARECEPTOR.
DR PROSITE: PS00237; G_PROTEIN_REC_P1.1; 1.
DR PROSITE: PS50262; G_PROTEIN_REC_P1.2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Phosphorylation; Lipoprotein; Palmitate.
FT DOMAIN 1 50 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 51 75 1 (POTENTIAL).
FT DOMAIN 76 82 2 (POTENTIAL).
FT TRANSMEM 83 111 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 112 125 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 126 144 3 (POTENTIAL).
FT DOMAIN 145 163 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 164 189 4 (POTENTIAL).
FT DOMAIN 190 205 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 206 226 5 (POTENTIAL).
FT DOMAIN 227 258 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 259 280 6 (POTENTIAL).
FT DOMAIN 281 294 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 295 315 7 (POTENTIAL).
FT DOMAIN 316 364 CYTOPLASMIC (POTENTIAL).
FT LIPID 327 327 PALMITATE (BY SIMILARITY).
FT CARBOHYD 27 27 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 35 35 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 340 340 S -> G (IN REF. 2).
SQ SEQUENCE 364 AA; 59E7722FD00DE74 CRC64;

Query Match
Best Local Similarity 22.3%; Score 438; DB 1; Length 364;
Matches 111; Conservative 54; Mismatches 152; Indels 18; Gaps 6;

OY 1 MNATGTPVAPESCOOLAAG-----HSRLIVYHNSGR-LAGRGPDGGIGALRGSLV 54
DB 1 MAISTSIIVISQPFQFMANNEQCYNESIAFYNRSGKHLATENYTS---KLWVGIGI 57
OY 55 AASCLVIVENLLVLAITSHMSRRVYVYCLVNTITLSDLTGAAVLAVNLGSGATFPLA 114
DB 58 TVCIFIMLANLIVVAIYVNRFRPIYVLANLAADFFGLAFYLMFTMGPTRLTJ 117
OY 115 PAQWFLREGILFTALAASTFSLFTAGERFANVRPAVESGATKTSRYGFIGLWLLAA 174
DB 118 VSTWLLRQGLIDTSLTASVAVNLATAIERHITVFERMQLHT-RMSNRVVVIVVITWMAI 176
OY 175 LIGMLPLIGMNCIAFDRCSSLLPLYSKRYILFCIVFAGVLATMGVGAIFRLVQASG 234
DB 177 VMGALPSVGMNCICDIENCSNMALPYSYLVEFMAIFLVFVYVVAIAIIFGVKQRT 236
OY 235 QKAPPAARRRRR-----LKTIVMILALFVCGPLGLLLADVFGSNMAQEYLRGM 289
DB 237 MKMSHSGGPRNRDPTMSLLKTVIVYIGAFIICWTPLGLVLLDVCCPQCDVLAVER- 294
OY 290 DWILALAVLSAVNPDIYSFRSREVCRAVLSFLCC 324
DB 295 -FELLAFENSAMNPDIYSYDRKESAFRQILCC 328

RESULT 9
EDG2_BOVIN STANDARD; PRT; 364 AA.
AC Q28031.
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Lysophosphatidic acid receptor (EDG-2) (Ref. 3).
GN EDG2.
```

```
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=97165887; PubMed=9013780;
RA Macrae A.D., Premont R.T., Jaber M., Petersen A.S., Lefkowitz R.J.;
RT "Cloning, characterization, and chromosomal localization of rec1.3, a
RT member of the G-protein-coupled receptor family highly expressed in
RT brain.";
RL Brain Res. Mol. Brain Res. 42:245-254(1996).
CC -!- FUNCTION: RECEPTOR FOR LYSOPHOSPHATIDIC ACID (LPA), A MEDIATOR OF
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U48236; AAC4695.1; -
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR InterPro: IPR004065; LPareceptor.
DR Pfam: PF00001; 7tm.1; 1.
DR PRINTS: PR01527; LPARECEPTOR.
DR PROSITE: PS00237; G_PROTEIN_REC_P1.1; 1.
DR PROSITE: PS50262; G_PROTEIN_REC_P1.2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Phosphorylation; Lipoprotein; Palmitate.
FT DOMAIN 1 50 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 51 75 1 (POTENTIAL).
FT DOMAIN 76 82 2 (POTENTIAL).
FT TRANSMEM 83 111 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 112 125 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 126 144 3 (POTENTIAL).
FT DOMAIN 145 163 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 164 189 4 (POTENTIAL).
FT DOMAIN 190 205 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 206 226 5 (POTENTIAL).
FT DOMAIN 227 258 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 259 280 6 (POTENTIAL).
FT DOMAIN 281 294 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 295 315 7 (POTENTIAL).
FT DOMAIN 316 364 CYTOPLASMIC (POTENTIAL).
FT LIPID 327 327 PALMITATE (BY SIMILARITY).
FT CARBOHYD 27 27 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 35 35 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 364 AA; 41070 MW; DE94675BA407B2F6 CRC64;

Query Match
Best Local Similarity 22.0%; Score 432.5; DB 1; Length 364;
Matches 103; Conservative 51; Mismatches 140; Indels 11; Gaps 4;

OY 25 IVLHYNSGRLAAGSGPDGGLALRGLSAVASCIVLENLIVLAITSHMSRRVYVC 84
DB 30 IAFVYNSRGKYLATENNTYTKL--VNGIGITVCIIFIMLANLIVVAIYVNRFRHPIYTL 87
OY 85 LVNITISDLITGAAIYLANVLSGARTFRLAPQWFLRBLFTALAASTFSLFTAGERE 144
DB 88 MANLAADEFAGLAFYLYMFNTPNTRRLTVSWLLRQGLIDTSLVSVANLATAIERH 147
OY 145 ATWVRPAESGATKTSRYVFGIGLWLLAALGMLPLIGMNCIAFDRCSSLLPLYSKRY 204
DB 148 IITFR-MQLHARSNRRVYVIVITMAIYMGALPSVGMNCICDIENCSNMALPYSQY 206
OY 205 IIFCLVIFAGVLATMGVGAIFRLVQASGOKAPPAARRRRR-----LKTIVMILLA 259
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DB 207 LVEFMAIFNLVTFVVVAVVLAHIFGVYRQRTMRMSSHSGSPRRNDPMASLKTIVYIVGA 266
OY 260 FLVCMGPFLGILLADVFGSNLMAOEYLKGMWILALAVLSAVNPITYSFRSREVCRAVL 319
DB 267 FLICHTPGVILLVLLDVCPGQCVLAVER---FFLLAFNSAMNPITYSYDKESATFR 323
OY 320 SFLCC 324
DB 324 QILCC 328

RESULT 10
CBIR_MOUSE STANDARD: PRT: 473 AA.
ID CBIR_MOUSE P47746;
AC 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Cannabinoid receptor 1 (CB1) (CB-R) (Brain-type cannabinoid receptor).
GN CNR1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RC SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=96272305; PubMed=8777318;
RX Chakrabarti A., Onalvi E.S., Chaudhuri G.;
RT "Cloning and sequencing of a cDNA encoding the mouse brain-type
RT cannabinoil receptor protein."
RL DNA Seq. 3:385-388(1995).
RN [2]
RC SEQUENCE FROM N.A.
RC STRAIN=129;
RA Bonner T.I.;
RL Submitted (MAR-1995) to the EMBL/genbank/DBJ databases.
RN [3]
RC SEQUENCE FROM N.A.
RX MEDLINE=96429553; PubMed=8832654;
RA Ho B.-Y., Zhao J.;
RT "Determination of the cannabinoid receptors in mouse x rat hybridoma
RT NG108-15 cells and rat G4C1 cells."
RL Neurosci. Lett. 212:123-126(1996).
RN [4]
RC SEQUENCE FROM N.A.
RA Yuan Z.-Q., Li L., Qiu B.-S., Song D.-K.;
RT "cDNA cloning and expression analysis of mouse cannabinoid receptor
RT (CB1) gene."
RL Submitted (MAY-1999) to the EMBL/genbank/DBJ databases.
RN [5]
RC SEQUENCE FROM N.A.
RC STRAIN=129/SV;
RX MEDLINE=99105999; PubMed=9888857;
RA Ledert C., Valverde O., Cosu G., Petitot F., Aubert J.F., Beslot F.,
RA Boehne G.A., Imperato A., Pedrazzini T., Roques B.P., Vassart G.,
RA Fratta W., Parmentier M.;
RT "Unresponsiveness to cannabinoids and reduced addictive effects of
RT opiates in CB1 receptor knockout mice."
RL Science 283:401-404(1999).
CC -1- FUNCTION: INVOLVED IN CANNABINOID-INDUCED CNS EFFECTS. ACTS BY
CC INHIBITING ADENYLYLATE CYCLASE. COULD BE A RECEPTOR FOR ANANDAMIDE.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC -----
DR EMBL: U17985; AAA57202.1; -
DR EMBL: U22948; AAA54413.1; -
DR EMBL: U40709; AAA91176.1; -
DR EMBL: AF153345; AAD34624.1; -
DR EMBL: Y18374; CAB42647.1; -
DR MGD: MGI:104615; Cnr1.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm.1.1.
DR PROSITE: PS00237; G_PROTEIN_RECP_F1_1; 1.
DR PROSITE: PS50262; G_PROTEIN_RECP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 117
FT TRANSSEM 118 143
FT DOMAIN 144 155
FT TRANSSEM 156 176
FT DOMAIN 177 188
FT TRANSSEM 189 213
FT DOMAIN 214 233
FT TRANSSEM 234 256
FT DOMAIN 257 274
FT TRANSSEM 275 300
FT DOMAIN 301 345
FT TRANSSEM 346 366
FT DOMAIN 367 378
FT TRANSSEM 379 400
FT DOMAIN 401 473
FT CARBOHYD 78 78
FT CARBOHYD 84 84
FT CONFLICT 9 9
FT CONFLICT 115 115
FT CONFLICT 211 211
SO SEQUENCE 473 AA; 52830 MW; E504168191CB6429 CRC64;
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Query Match 17.98; Score 351; DB 1; Length 473;
Best Local Similarity 30.18; Pred. No. 1,6e-16;
Matches 105; Conservative 61; Mismatches 129; Indels 54; Gaps 11;
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OY 48 ALRGISVAASCLVVENLVLAATITSHMRSRW--VYCVLNTITSLDGLGAAYLANVLL 105
DB 119 ALAVSLTGLTFVLENLVLCVIL-HSRILRCRPSHFISGLAVADLGSVIFYVSFD 177
OY 106 SGARTFLPAPQWFLREGLFTALASTFSLLFTAGSRFPAWVPA-ESGATKTSVYG 164
DB 178 FHFVFRKDSFVFLFKLGVTASFTASGSLFLAIRYISIHRLPAYKRIYVRPAVA 237
OY 165 FTGLCMILALLGMLPLIGMNCICAFDRCSLLFLYSKRYLFLCTVFAGVATIMGLG 224
DB 238 FC-LMWTIAIVAVLPLGMCKKLOSVCSDIFPLIDETIYIMFIVGTSVLLFIYAVM 296
OY 225 AIF-----RLVQASGOKA-----PRPAARRKARLLKTYLMLILAEVLC 263
DB 297 YILMKASHAVRMIGRGRGKSIITHSBDKVGQYTRPDQARMDRLAKTVLLIVLIIIC 356
OY 264 WGPLFGLLADVFGSNLMAOEYLKGMWIL-----ALAVLSAVNPITYSFRSREVC 315
DB 357 WGPLLAIVYDVFGK-----MNLKITYFAFCSMCLLNSVNPITYALRSKDLR 406
OY 316 RAVLSFL--CCGCLRL--GMRPGDCLARAFAVHSGASTDSLRPDS 360
DB 407 HAFNSMFPSCREGTAQPLDNSMGDSDEL-----HKHANNTASMRRAES 449

RESULT 11
CBIR_RAT STANDARD: PRT: 473 AA.
ID CBIR_RAT P20272;
AC 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Cannabinoid receptor 1 (CB1) (CB-R) (Brain-type cannabinoid receptor).
GN CNR1 OR SKR6.
OS Rattus norvegicus (Rat).
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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain cortex;
RX MEDLINE=90332039; PubMed=2165569;
RA Matsuda L.A., Lolait S.J., Brownstein M.J., Young A.C., Bonner T.I.;
RT "Structure of a cannabinoid receptor and functional expression of the
RT cloned cDNA.";
RL Nature 346:561-564(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96429553; PubMed=8832654;
RA Ho B.Y., Zhao J.;
RT "Determination of the cannabinoid receptors in mouse x rat hybridoma
RT NG108-15 cells and rat GH41 cells.";
RL Neurosci. Lett. 212:123-126(1996).
CC -1- FUNCTION: INVOLVED IN CANNABINOID-INDUCED CNS EFFECTS. ACTS BY
CC -1- INHIBITING ADENYLATE CYCLASE. COULD BE A RECEPTOR FOR ANANDAMIDE.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC -----
CC EMBL; X55812; CAA9332.1; -
CC DR EMBL; U40395; AAA99067.1; -
CC DR PIR; A33117; A33117.
CC DR InterPro: IPR002276; GPCR_Rhodpsn.
CC DR Pfam: PF00001; 7tm_1; 1
CC DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
CC DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
CC KW G-protein coupled receptor; Transmembrane; Glycoprotein.
CC FT DOMAIN 1 117
CC FT TRANSSEM 118 143
CC FT DOMAIN 144 155
CC FT TRANSSEM 156 176
CC FT DOMAIN 177 188
CC FT TRANSSEM 189 213
CC FT DOMAIN 214 233
CC FT TRANSSEM 234 256
CC FT DOMAIN 257 274
CC FT TRANSSEM 275 300
CC FT DOMAIN 301 345
CC FT TRANSSEM 346 366
CC FT DOMAIN 367 378
CC FT TRANSSEM 379 400
CC FT DOMAIN 401 473
CC FT CARBOHYD 78
CC FT CARBOHYD 84
CC SEQUENCE 473 AA; 52845 MW; E59A66FAE17B646C CRC64;
Query Match 17.9%; Score 351; DB 1; Length 473;
Best Local Similarity 30.1%; Pred. No. 1.6e-16;
Matches 105; Conservative 61; Mismatches 129; Indels 54; Gaps 11;
```

```
OY 225 AIF-----RLVQASGQRA-----PPAARARRRLKTLVIMTLAFLVC 263
DB 297 YILMKASHAVRMIOFGTOXSIITHTSEDKVOYTRPDQARMIDRIAKTVLTLVLLIC 356
OY 264 WGPLEGLLADVFGSNMAQGYLRGMDIL-----ALAVINSAVNPIYSFRSREVC 315
DB 357 WGPLALINVVYVFGK-----MKKLKTYAFQFSMCLLNSVNPPIYALFRSKDR 406
OY 316 RAVLSFL--CCGCLRL--GMRPGDCIARAVEAHSGASTDSSLRPRDS 360
DB 407 HAFRSMFSPSCGTQAPLDNSMGDSDDL-----HKHANNATSMHRAAES 449
RESULT 12
CB1B_FUGRU STANDARD; PRT; 470 AA.
AC 098895;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Cannabinoid receptor type 1B.
DE CB1B.
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Takifugu.
OX NCBI_TaxID=31033;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=97001167; PubMed=8812500;
RA Yamaguchi F., Macrae A., Brenner S.;
RT "Molecular cloning of two cannabinoid type 1-like receptor genes from
RT the puffer fish Fugu rubripes.";
RL Genomics 35:603-605(1996).
CC -1- FUNCTION: INVOLVED IN CANNABINOID-INDUCED CNS EFFECTS (POTENTIAL).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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CC -----
CC EMBL; X94402; CAA64175.1; -
CC DR InterPro: IPR002276; GPCR_Rhodpsn.
CC DR Pfam: PF00001; 7tm_1; 1.
CC DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
CC DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
CC KW G-protein coupled receptor; Transmembrane; Glycoprotein.
CC FT DOMAIN 1 113
CC FT TRANSSEM 114 139
CC FT DOMAIN 140 151
CC FT TRANSSEM 152 172
CC FT DOMAIN 173 184
CC FT TRANSSEM 185 209
CC FT DOMAIN 210 229
CC FT TRANSSEM 230 252
CC FT DOMAIN 253 270
CC FT TRANSSEM 271 296
CC FT DOMAIN 297 341
CC FT TRANSSEM 342 362
CC FT DOMAIN 363 374
CC FT TRANSSEM 375 396
CC FT DOMAIN 397 470
CC FT CARBOHYD 78
CC FT CARBOHYD 86
CC SEQUENCE 470 AA; 52081 MW; CE87C037FDF9192 CRC64;
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Query Match 17.6%; Score 346.5; DB 1; Length 470;
 Best Local Similarity 28.2%; Pred. No. 3.2e-16;
 Matches 95; Conservative 70; Mismatches 129; Indels 43; Gaps 9;

QY 52 LVAASCLVLENLVLAIT-SHMSRRMYVYCVNTLSLDTLGAAYLANVLLSGART 110
 D 119 LATTGTFLENFVLCVILSHSLRSPSYHFGISLAVADLLGSIIFVYSFIDFVHL 178
 QY 111 FLAPAWFLREGLEFTALASTFSLTFAGRFATMPVPA-ESGATKTSRYVG 169
 D 179 RKSPSFLFKLAGVIASTASVGSFLTAIDRYSHRPAVYRIITKRAVIAF-SVM 237
 QY 170 WLTAALGLMPLLGWNCICAFDRCSLLPLYSKRYIFLCVIFAGVATIMGLYALF-- 227
 D 238 MAISIERSLPILGWNCKRLHSVCSDFIPLDKRYIMFWIMGTVLLFIYAYMFLMK 297
 QY 228 -----RLVOASGOKA-----PRPARRRARLLKTVMLILAFVCGPDLF 268
 D 298 SHHAAVAMLSRSSQKSIITYTSEGTRVOTVREPARMDRLAKTLVLVLAIIICWGPL 357
 QY 269 GLLADVFGSNLMAOEYLRGMWMLA-----LAVLSAVNPITYFSRREVCRAVLSF 321
 D 358 AIVWYDLFG-----RVNDFIKTVAFSCMLCLINSTINPVYAMRSKDLRARAVNI 408
 QY 322 --LCGCGCLR-LGMRGPDCLARAVAHGASATDSSL 355
 D 409 CHMCRGTTQSLDSSAESDMNSKRSVSTGGRAGKDRSV 445

RESULT 13
 CBIR_FELCA STANDARD; PRT: 472 AA.
 ID CBIR_FELCA AC 002777;
 DT 15-JUL-1998 (rel. 36, Created)
 DT 15-JUL-1998 (rel. 36, Last sequence update)
 DT 16-OCT-2001 (rel. 40, Last annotation update)
 DE Cannabinoid receptor 1 (CB1) (CB-R).
 GN CNR1.
 OS Felis silvestris catus (Cat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
 OX NCBI_TaxID=9685;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Gebremedhin D., Lange A.R., Aebly M.R., Campbell W.B., Hillard C.J.,
 RA Harder D.R.;
 RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: INVOLVED IN CANNABINOID-INDUCED CNS EFFECTS. ACTS BY
 CC INHIBITING ADENYLYATE CYCLASE. COULD BE A RECEPTOR FOR ANANDAMIDE.
 CC INHIBITS L-TYPE CA2+ CHANNEL CURRENT.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN CEREBRAL ARTERIAL MUSCLE CELLS.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 CC -----
 CC EMBL: 094342; AAB53440.1;
 DR InterPro: IPR000276; GPCR_Rhodpsn.
 DR Pfam: PF00001; 7tm_1; 1
 DR PROSITE: PS00237; G_PROTEIN_RECPT_F1_1; 1.
 DR PROSITE: PS50262; G_PROTEIN_RECPT_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 1 116
 FT TRANSMEM 117 142
 FT DOMAIN 143 154
 FT TRANSMEM 155 175
 FT 2 (POTENTIAL).

FT DOMAIN 176 187
 FT TRANSMEM 188 212
 FT DOMAIN 213 232
 FT TRANSMEM 233 252
 FT DOMAIN 256 273
 FT TRANSMEM 274 299
 FT DOMAIN 300 344
 FT TRANSMEM 345 365
 FT DOMAIN 366 377
 FT TRANSMEM 378 399
 FT DOMAIN 400 472
 FT CARBOHYD 77 77
 FT CARBOHYD 83 83
 SO SEQUENCE 472 AA; 52887 MW; A2774DBF82DAF34 CRC64;

Query Match 17.5%; Score 345; DB 1; Length 472;
 Best Local Similarity 30.0%; Pred. No. 4e-16;
 Matches 102; Conservative 60; Mismatches 124; Indels 54; Gaps 11;

QY 48 ALRGLVAAASCLVLENLVLAITSHMSRRM--VYCVLVNTLSLDTLGAAYLANVL 105
 D 118 AIAVLSLTGTFVLENLVLCVIL-HSRSLCRSPSYHFGISLAVADLLGSIIFVYSFVD 176
 QY 106 SGATFPLAPAWFLREGLEFTALASTFSLTFAGRFATMPVPA-ESGATKTSRYVG 164
 D 177 FHVHRDQSNVFLFKIGVYTSFASVGSFLTAIDRYSHRPAVYRIITKRAVIAF 236
 QY 165 FIGLWLLAALGLMPLLGWNCICAFDRCSLLPLYSKRYIFLCVIFAGVATIMGLY 224
 D 237 FC-LMTTIAIVIAVPLPLGNCCKRLQSVCSDFIPLDIETVIMFWIGVSVLLFIYAYM 295
 QY 225 AIF-----RLVOASGOKA-----PRPARRRARLLKTVMLILAFVCG 263
 D 296 YILMKAIHAAVNRQKSTIITYTSEGTRVOTVREPARMDRLAKTLVLVLAIIICW 355
 QY 264 WGPLFGLLADVFGSNLMAOEYLRGMWMLA-----LAVLSAVNPITYFSRREVC 315
 D 356 WGPLLAIMVYDVEFG-----MNKLIKTVAFSCMLCLINSTINPVYIYALRSKDLR 405
 QY 316 RAVLSFL--CCGCLR--GMRGPDCLARAVAHGASATD 351
 D 406 HAFRSMFSCGEGTAQPLDMSKGDSDL-----HKHANVT 439

RESULT 14
 EDGL_MOUSE STANDARD; PRT: 180 AA.
 ID EDGL_MOUSE AC P52592;
 DT 01-OCT-1996 (rel. 34, Created)
 DT 01-OCT-1996 (rel. 34, Last sequence update)
 DT 15-JUL-1998 (rel. 36, Last annotation update)
 DE Probable G protein-coupled receptor EDG-1 like (Fragment).
 GN GPCR13.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA TISSUE-Testis;
 RX MEDLINE=94116980; PubMed=8288218;
 RA Wilkie T.M., Chen Y., Gilbert D.J., Moore K.J., Yu L., Simon M.I.,
 RA Copeland N.G., Jenkins N.A.;
 RL "Identification, chromosomal location, and genome organization of
 RL mammalian G-protein-coupled receptors";
 RL Genomics 18:175-184(1993).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way

FT FT /note= "transmembrane domain IV"
 FT Domain 183..199
 FT /note= "extracellular domain EL-II"
 FT Domain 200..224
 FT /note= "transmembrane domain V"
 FT Domain 225..250
 FT /note= "intracellular domain IL-III"
 FT Domain 251..272
 FT /note= "transmembrane domain VI"
 FT Domain 273..285
 FT /note= "extracellular domain EL-III"
 FT Domain 286..304
 FT /note= "transmembrane domain VII"
 FT Modified-site 2
 FT /note= "N-glycosylated"
 FT Modified-site 30
 FT /note= "N-glycosylated"
 FT Modified-site 77
 FT /note= "O-phosphorylated"
 FT Modified-site 159
 FT /note= "O-phosphorylated"
 FT Modified-site 308
 FT /note= "O-phosphorylated"
 FT Modified-site 360
 FT /note= "O-phosphorylated"
 FT Modified-site 380
 FT /note= "O-phosphorylated"
 FT Modified-site /note= "O-phosphorylated"
 PN MO9935106-A2.
 XX 15-JUL-1999.
 PD 30-DEC-1998; 98WO-CA01196.
 XX 30-DEC-1998;
 PF 30-DEC-1997; 97US-0070184.
 PR 30-DEC-1997;
 XX (ALIX) ALIELIX BIOPHARMACEUTICALS INC.
 PA Gupta AK, Munroe DG, Zastawny RL;
 PI WPI: 1999-419322/35.
 XX N-PSDB: AAX59366.
 DR A nucleic acid sequence encoding human EDG-7 receptor, useful for
 XX treating disorders associated with aberrant expression
 PT Claim 12; Fig 2A; 72pp; English.
 XX
 PS The present sequence represents a novel human homologue of the
 CC EDG-7 receptor, i.e. HEDG-7, a 7-transmembrane G protein coupled
 CC receptor. The sequence is predicted from isolated BAC and PAC
 CC clones (see AAX59366) and differs at only 2 amino acid residues
 CC (140 and 178) from the sequence (see AAY06412) from an isolated
 CC cDNA clone. Also claimed are an expression vector comprising a
 CC HEDG-7 nucleotide sequence, a host cell, and methods of using
 CC HEDG-7 receptor to identify potential HEDG-7 ligands and
 CC antagonists. Ligands, agonists and antagonists of HEDG-7 may
 CC be useful for detecting inflammation or disease associated with
 CC abnormal levels of HEDG-7 expression. Detection of aberrant
 CC expression of HEDG-7 can accelerate diagnosis and proper treatment
 CC of abnormal conditions, e.g. adult respiratory distress, asthma,
 CC rheumatoid arthritis, cardiac ischaemia, acute pancreatitis, septic
 CC shock, psoriasis, acute cyclosporin nephrotoxicity and early
 CC diabetic glomerulopathy, as well as lung damage following exposure
 CC to cigarette smoke, asbestos or silica.
 XX
 SQ Sequence 384 AA;
 Query Match 100.0%; Score 1966; DB 20; Length 384;
 Best Local Similarity 100.0%; Pred. No. 2, 4e-206;
 Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MNATGTPVAPESCCQOLAAGHSRLIVLHYNHSRGLRAGGPEDEGCLGALGLSYAASCLV 60
 QY 61 VLENILVLAATITSHMRSRWYCYCLVNTITSDLTGAAYLANVLSCARFRLAPQWFL 120
 Db 61 VLENILVLAATITSHMRSRWYCYCLVNTITSDLTGAAYLANVLSCARFRLAPQWFL 120
 QY 121 REGLEFTRALASTFSLFTAGERFATWVPVPAESGATKTSRVYGFGLCMLLAALGMLP 180
 Db 121 REGLEFTRALASTFSLFTAGERFATWVPVPAESGATKTSRVYGFGLCMLLAALGMLP 180
 QY 181 LLGNMCIAPDRCSLLPLYSKRYILFCVIFAGVATITNGLYGATFRLVQASGQAPRP 240
 Db 181 LLGNMCIAPDRCSLLPLYSKRYILFCVIFAGVATITNGLYGATFRLVQASGQAPRP 240
 QY 241 AARRKARLKTVMITLAPLCVCGPFLGILLADVFESNMAQETLGMVITLAVLNS 300
 Db 241 AARRKARLKTVMITLAPLCVCGPFLGILLADVFESNMAQETLGMVITLAVLNS 300
 QY 301 AVNPITISFRSREYCAVLSFLCCGCLRLGMRGPGDCLARAVEHSGASTTDSLRPRS 360
 Db 301 AVNPITISFRSREYCAVLSFLCCGCLRLGMRGPGDCLARAVEHSGASTTDSLRPRS 360
 QY 361 FRGSRSLSFRRREPLSISSVRSI 384
 Db 361 FRGSRSLSFRRREPLSISSVRSI 384
 RESULT 2
 AAY69500
 ID AAY69500 standard; Protein; 384 AA.
 XX AAY69500;
 AC 12-JUL-2000 (first entry)
 DT A human G-protein coupled receptor designated 14275 receptor.
 XX Human: G-protein coupled receptor; GPCR; EDG receptor; 14275 receptor;
 KW signalling pathway; GPCR-mediated disorder; anaemia; neutropenia;
 KM thrombocytopenia; inflammation.
 XX Homo sapiens.
 OS
 FH Key
 FT Domain
 FT Location/Qualifiers
 FT 1..50
 FT /note= "extracellular domain"
 FT 2..5
 FT /note= "N glycosylation site"
 FT 30..33
 FT /note= "N glycosylation site"
 FT /note= "transmembrane segment"
 FT 32..34
 FT /note= "protein kinase C phosphorylation site"
 FT 44..49
 FT /note= "N-myristoylation site"
 FT 51..56
 FT /note= "N-myristoylation site"
 FT Domain
 FT 51..331
 FT /note= "transmembrane domain"
 FT 51..71
 FT /note= "transmembrane segment"
 FT 77..79
 FT /note= "protein kinase C phosphorylation site"
 FT 81..105
 FT /note= "transmembrane segment"
 FT 87..90
 FT /note= "N glycosylation site"
 FT 89..92
 FT /note= "casein kinase II phosphorylation site"
 FT 110..112
 FT /note= "protein kinase C phosphorylation site"
 FT 123..141
 FT Region

Seq	Sequence	384 AA
Query Match	100.0%;	Score 1966; DB 21; Length 384;
Best Local Similarity	100.0%;	Pred. No. 2,4e-206;
Matches 384;	Conservative 0;	Mismatches 0; Indels 0; Gaps
OY	1	MAATGTPVAPESCCQLAAGSHRLIVLHYNHSGRLAGRGPEDEGGLGALRGLSVAASCLV 60
Db	1	MAATGTPVAPESCCQLAAGSHRLIVLHYNHSGRLAGRGPEDEGGLGALRGLSVAASCLV 60
OY	61	VLENLVLVAITSHMRSRWVYVCLVNTITLSDLLTGAAYLANVLLSGARTFRLAPQWFL 120
Db	61	VLENLVLVAITSHMRSRWVYVCLVNTITLSDLLTGAAYLANVLLSGARTFRLAPQWFL 120
OY	121	REELFTTALAASFEISLFTAGEAPATMVPPVAESGATKTSVYGFISLCLWLLAALIGMLP 180
Db	121	REELFTTALAASFEISLFTAGEAPATMVPPVAESGATKTSVYGFISLCLWLLAALIGMLP 180
OY	181	LIGMNCALCFDRCSSLEPLYSKRIYIFCLVIFAGVATITMGLYCAITRIVQASGKAPRP 240
Db	181	LIGMNCALCFDRCSSLEPLYSKRIYIFCLVIFAGVATITMGLYCAITRIVQASGKAPRP 240
OY	241	AARRKRRLLKTVLMLIILAFVYCGPLFGLLLADYFGSNLMAOXYLRGMDIILAVLNS 300
Db	241	AARRKRRLLKTVLMLIILAFVYCGPLFGLLLADYFGSNLMAOXYLRGMDIILAVLNS 300
OY	301	AVNPITYSFRSREVCRAVLSFLCCGCLRLGMNGPGDCLARAVEHSGASTTDSLRPDS 360
Db	301	AVNPITYSFRSREVCRAVLSFLCCGCLRLGMNGPGDCLARAVEHSGASTTDSLRPDS 360
OY	361	FRGSRSLSFMRREPLSSISSVRSI 384
Db	361	FRGSRSLSFMRREPLSSISSVRSI 384
RESULT 3		
AAW90862		
ID	AAW90862	standard; Protein; 384 AA.
AC	AAW90862;	
XX	29-JUN-2000	(first entry)
DE	Human edg6 protein.	
XX	edg6; human; G-coupled receptor; endothelial differentiation gene;	
KW	antitumorigenic; immunomodulatory; antimicrobial; antiallergic;	
KW	cytotoxic; gene therapy; inflammation; autoimmune disease; allergy;	
KW	tumor; leukemia; lymphoma.	
OS	Homo sapiens.	
XX	DE19846979-A1.	
XX	23-MAR-2000.	
XX	13-OCT-1998;	98DE-1046979.
XX	11-SEP-1998;	98DE-1043240.
XX	(DELB-) DELBROECK CENT MOLEKULARE MEDIZIN MAX.	
XX	Graeler M, Bernhardt G, Lipp M;	
XX	WPI; 2000-258069/73.	
XX	N-PDB; AAX82789.	
PT	New human and murine G-coupled receptor EDG (endothelial	
PT	differentiation gene) 6, useful for modulating inflammatory and immune	
PT	reactions and for treatment of allergy or tumors	
XX	Claim 1; Page 6; 12pp; German.	

CC This invention describes novel human and murine G-coupled receptors EDG
CC (endothelial differentiation gene) 6 (I and II). The products of the
CC invention have antiinflammatory, immunomodulatory, antimicrobial,
CC antiallergic and cytostatic activity. (I) and (II) are involved in signal
CC transduction. (I), (II) and their fragments, variants and mutants or
CC binding partners, are used therapeutically to modulate the function of
CC blood and body cells, particularly for inhibition of acute and chronic
CC inflammation and to raise specific antibodies against them. They are used
CC as a source of diagnostic oligonucleotides and for gene therapy.
CC Antibodies against (I) and (II) are useful for diagnosis and optionally
CC when coupled to therapeutic agents, toxins or other antibodies, to
CC modulate immune and inflammatory responses for example immunological
CC defects such as inflammation, infection, autoimmune diseases, allergy,
CC tumors, leukemia and lymphoma. This sequence represents the human EDG6
CC protein described in the method of the invention.

CC
XX
SQ Sequence 384 AA:

Query Match 100.0%; Score 1966; DB 21; Length 384;
Best Local Similarity 100.0%; Pred. No. 2.4e-206;
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNATGTPVAPESCOQLAAGHSRLIVLHYNHSGRLAGRGPEDEGLGALRGLSVAASCLV 60
DB 1 MNATGTPVAPESCOQLAAGHSRLIVLHYNHSGRLAGRGPEDEGLGALRGLSVAASCLV 60
QY 61 VLENLLVLAITSHMRSRRWYVCVNTITSDLTGAAYLANVLSGARFRLAPAOEWL 120
DB 61 VLENLLVLAITSHMRSRRWYVCVNTITSDLTGAAYLANVLSGARFRLAPAOEWL 120
QY 121 REGILFTALAASTFSLFTAGERFATWVPVASEGATKTSRYVIGICWMLAALGMLP 180
DB 121 REGILFTALAASTFSLFTAGERFATWVPVASEGATKTSRYVIGICWMLAALGMLP 180
QY 181 LIGWNCICAFDRCSLLPIYSKRYILFCLVIFAGVLAITMGLYGAIFRLVQASQKAPRP 240
DB 181 LIGWNCICAFDRCSLLPIYSKRYILFCLVIFAGVLAITMGLYGAIFRLVQASQKAPRP 240
QY 241 AARRKARRLKTYMLLAFVLCWGPFLGILLADVFSGNLMAOEYLRGMIMLAVLNS 300
DB 241 AARRKARRLKTYMLLAFVLCWGPFLGILLADVFSGNLMAOEYLRGMIMLAVLNS 300
QY 301 AVNPITISFRSREVCRAVLSFLCCGCLRIGMGPDCLARAVEHSGASTTSSLRPDS 360
DB 301 AVNPITISFRSREVCRAVLSFLCCGCLRIGMGPDCLARAVEHSGASTTSSLRPDS 360
QY 361 FRGSRSLSPMRREPLSSISVSRSI 384
DB 361 FRGSRSLSPMRREPLSSISVSRSI 384

RESULT 4
AAM48981 ID AAM48981 standard; Protein; 384 AA.
AC AAM48981;
XX
XX 26-APR-2002 (first entry)
XX Human endothelial differentiation, G-protein coupled receptor 6.
XX
XX Human; endothelial differentiation, G-protein coupled receptor 6;
XX EDG6; haplotype; cancer; angiogenesis; inflammation; chromosome 19p13.3;
XX cytostatic; antiinflammatory; gene therapy; SNP;
XX single nucleotide polymorphism.
OS Homo sapiens.
XX
XX
XX Key Location/Qualifiers
XX Misc-difference 155 /note= "optionally Arg"
XX Misc-difference 164 /note= "optionally Ser"
XX
XX
XX
XX

FT Misc-difference 198 /note= "optionally Ser"
FT Misc-difference 243 /note= "optionally Cys"
FT Misc-difference 365 /note= "optionally Leu"
FT Misc-difference 381 /note= "optionally Met"
XX
XX W0200206446-A2.
XX
XX 24-JAN-2002.
XX
XX 17-JUL-2001; 2001WO-US22523.
XX
XX 17-JUL-2000; 2000US-218727P.
XX
XX (GENA-) GENNISSANCE PHARM INC.
XX
XX Kitem SE, Koshy B;
XX
XX WPI: 2002-171804/22.
XX N-PSDB; ABL45808, ABL45809.
XX
XX New genetic variants of endothelial differentiation, G-protein coupled
XX receptor-6 gene for studying expression, function of the gene and
XX expressing EDG6 protein for use in screening drugs to treat cancer,
XX inflammation -
XX
XX Claim 28; Fig 3; 11pp; English.

CC The present invention provides the gene, protein and cDNA sequences of
CC the human endothelial differentiation, G-protein coupled receptor 6
CC (EDG6). Also identified are single nucleotide polymorphisms (SNPs) found
CC within the sequences. The sequences can be used in the identification of
CC the haplotype of an individual, and in the treatment of cancer,
CC angiogenesis and inflammation. The present sequence is the EDG6 protein,
CC the gene for which is found on chromosome 19p13.3.

CC
XX
SQ Sequence 384 AA:

Query Match 100.0%; Score 1966; DB 23; Length 384;
Best Local Similarity 100.0%; Pred. No. 2.4e-206;
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNATGTPVAPESCOQLAAGHSRLIVLHYNHSGRLAGRGPEDEGLGALRGLSVAASCLV 60
DB 1 MNATGTPVAPESCOQLAAGHSRLIVLHYNHSGRLAGRGPEDEGLGALRGLSVAASCLV 60
QY 61 VLENLLVLAITSHMRSRRWYVCVNTITSDLTGAAYLANVLSGARFRLAPAOEWL 120
DB 61 VLENLLVLAITSHMRSRRWYVCVNTITSDLTGAAYLANVLSGARFRLAPAOEWL 120
QY 121 REGILFTALAASTFSLFTAGERFATWVPVASEGATKTSRYVIGICWMLAALGMLP 180
DB 121 REGILFTALAASTFSLFTAGERFATWVPVASEGATKTSRYVIGICWMLAALGMLP 180
QY 181 LIGWNCICAFDRCSLLPIYSKRYILFCLVIFAGVLAITMGLYGAIFRLVQASQKAPRP 240
DB 181 LIGWNCICAFDRCSLLPIYSKRYILFCLVIFAGVLAITMGLYGAIFRLVQASQKAPRP 240
QY 241 AARRKARRLKTYMLLAFVLCWGPFLGILLADVFSGNLMAOEYLRGMIMLAVLNS 300
DB 241 AARRKARRLKTYMLLAFVLCWGPFLGILLADVFSGNLMAOEYLRGMIMLAVLNS 300
QY 301 AVNPITISFRSREVCRAVLSFLCCGCLRIGMGPDCLARAVEHSGASTTSSLRPDS 360
DB 301 AVNPITISFRSREVCRAVLSFLCCGCLRIGMGPDCLARAVEHSGASTTSSLRPDS 360
QY 361 FRGSRSLSPMRREPLSSISVSRSI 384
DB 361 FRGSRSLSPMRREPLSSISVSRSI 384

RESULT 5
 ID AAY06412
 XX AAY06412 standard; Protein: 384 AA.
 AC AAY06412;
 DT 20-SEP-1999 (first entry)
 XX
 DE Human EDG-7 receptor homologue.
 XX
 KW EDG-7; human; HEDG-7; G protein coupled receptor; asthma;
 adult respiratory distress syndrome; rheumatoid arthritis;
 cardiac ischaemia; acute pancreatitis; septic shock; psoriasis;
 acute cyclosporin nephrotoxicity; diabetic glomerulopathy;
 lung damage; diagnosis; therapy; drug screening;
 antiinflammatory.
 KW
 OS Homo sapiens.
 XX
 FH Key
 FT Location/Qualifiers
 FT 50..70
 FT /note= "transmembrane domain I"
 FT 71..81
 FT /note= "intercellular domain IL-I"
 FT 82..105
 FT /note= "transmembrane domain II"
 FT 106..124
 FT /note= "extracellular domain EL-I"
 FT 125..143
 FT /note= "transmembrane domain IIT"
 FT 144..163
 FT /note= "intracellular domain IL-IIT"
 FT 164..182
 FT /note= "transmembrane domain IV"
 FT 183..199
 FT /note= "extracellular domain EL-IIT"
 FT 200..224
 FT /note= "transmembrane domain V"
 FT 225..250
 FT /note= "intracellular domain IL-IIT"
 FT 251..272
 FT /note= "transmembrane domain VI"
 FT 273..285
 FT /note= "extracellular domain EL-IIT"
 FT 286..304
 FT /note= "transmembrane domain VII"
 FT 2
 FT /note= "N-glycosylated"
 FT 30
 FT /note= "N-glycosylated"
 FT 77
 FT /note= "O-phosphorylated"
 FT 159
 FT /note= "O-phosphorylated"
 FT 308
 FT /note= "O-phosphorylated"
 FT 360
 FT /note= "O-phosphorylated"
 FT 380
 FT /note= "O-phosphorylated"
 FT
 XX MO935106-AZ.
 XX
 PD 15-JUL-1999.
 XX
 PE 30-DEC-1998; 98WC-CA01196.
 XX
 PR 30-DEC-1997; 97US-0070184.
 XX
 PA (ALIX) ALLELIX BIOPHARMACEUTICALS INC.
 XX
 PI Gupta AK, Munroe DG, Zastawny RL;

XX
 DR WPI: 1999-419322/35.
 DR N-PSDB; AAX59367.
 XX
 PT A nucleic acid sequence encoding human EDG-7 receptor, useful for
 PT treating disorders associated with aberrant expression
 XX
 PS Claim 12; Fig 2B; 72pp; English.
 XX
 CC The present sequence represents a novel human homologue of the
 CC EDG-7 receptor, i.e. HEDG-7, a 7-transmembrane G protein coupled
 CC receptor. The sequence is predicted from the cDNA insert of a
 CC Jurkat T-cell clone (see AAX59367) and differs at only 2 amino acid
 CC residues (140 and 178) from the sequence (see AAY06411) predicted
 CC from BAC and pMC clones. Also claimed are an expression vector
 CC comprising a HEDG-7 nucleotide sequence, a host cell, and methods
 CC of using HEDG-7 receptor to identify potential HEDG-7 ligands and
 CC antagonists. Ligands, agonists and antagonists of HEDG-7 may
 CC be useful for detecting inflammation or disease associated with
 CC abnormal levels of HEDG-7 expression. Detection of aberrant
 CC expression of HEDG-7 can accelerate diagnosis and proper treatment
 CC of abnormal conditions, e.g. adult respiratory distress, asthma,
 CC rheumatoid arthritis, cardiac ischaemia, acute pancreatitis, septic
 CC shock, psoriasis, acute cyclosporin nephrotoxicity and early
 CC diabetic glomerulopathy, as well as lung damage following exposure
 CC to cigarette smoke, asbestos or silica.
 CC
 XX
 SQ Sequence 384 AA;
 XX
 Query Match 99.5%; Score 1956; DB 20; Length 384;
 Best Local Similarity 99.5%; Pred. No. 3e-205;
 Matches 382; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 MNATGTPVAPESCCQQLAAGHSRLIVLHYNHSGRLAARGGPDGGLAGLSVAASCLV 60
 DB 1 MNATGTPVAPESCCQQLAAGHSRLIVLHYNHSGRLAARGGPDGGLAGLSVAASCLV 60
 QY 61 VLENILVLAATTSIMRSRWYVCLVNTTSDLLTGAAVLANVLLSGARFRLAPAQWL 120
 DB 61 VLENILVLAATTSIMRSRWYVCLVNTTSDLLTGAAVLANVLLSGARFRLAPAQWL 120
 QY 121 REGLEFTALASTPSILFTAGERFATWVPVASEGARTKSHVYFGLCMLAALLGMLP 180
 DB 121 REGLEFTALASTPSILFTAGERFATWVPVASEGARTKSHVYFGLCMLAALLGMLP 180
 QY 181 LLGNWCLCAFDRCSLLPLYSKRYILFCLVIFAGVLAITMGLYAFIRLVOASGQKARP 240
 DB 181 LLGNWCLCAFDRCSLLPLYSKRYILFCLVIFAGVLAITMGLYAFIRLVOASGQKARP 240
 QY 241 AARRKARRLKTVIMTLAFLVCWGPLFGLLADYFGSNLMAOYELGKMDIALLAVINS 300
 DB 241 AARRKARRLKTVIMTLAFLVCWGPLFGLLADYFGSNLMAOYELGKMDIALLAVINS 300
 QY 301 AVNPITVSPRSREVCRAVLSFLCCGCLRLGMRGPDCLARAVEAHSGASTDSSLRPDS 360
 DB 301 AVNPITVSPRSREVCRAVLSFLCCGCLRLGMRGPDCLARAVEAHSGASTDSSLRPDS 360
 QY 361 FRGSRSLSPRMREPLSSISVSRSI 384
 DB 361 FRGSRSLSPRMREPLSSISVSRSI 384
 XX
 RESULT 6
 AAW90863
 ID AAW90863 standard; Protein: 386 AA.
 XX
 AC AAW90863;
 XX
 DT 29-JUN-2000 (first entry)
 XX
 DE Murine edg6 protein.
 XX
 KW edg6; murine; G-coupled receptor; endothelial differentiation gene;

KM antiinflammatory; immunomodulatory; antimicrobial; antiallergic;
KM cytostatic; gene therapy; inflammation; autoimmune disease; allergy;
KM tumor; leukemia; lymphoma.
OS Mus sp.
XX DE19846979-A1.
XX 23-MAR-2000.
XX 13-OCT-1998; 98DE-1046979.
XX PF 13-OCT-1998; 98DE-1043240.
XX PR 11-SEP-1998; 98DE-1043240.
XX PA (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
XX PI Graeler M, Bernhardt G, Lipp M;
XX WPI: 2000-258069/23.
XX DR N-PSDB; AAX82790.
XX PT New human and murine G-coupled receptor EDG (endothelial
XX differentiation gene) 6, useful for modulating inflammatory and immune
XX reactions and for treatment of allergy or tumors -
XX PS Claim 2; Page 6; 12pp; German.
XX CC This invention describes novel human and murine G-coupled receptors EDG
XX (endothelial differentiation gene) 6 (I and II). The products of the
XX invention have antiinflammatory, immunomodulatory, antimicrobial,
XX antiallergic and cytostatic activity. (I) and (II) are involved in signal
XX transduction. (I), (II) and their fragments, variants and mutants or
XX binding partners, are used therapeutically to modulate the function of
XX blood and body cells, particularly for inhibition of acute and chronic
XX inflammation and to raise specific antibodies against them. They are used
XX as a source of diagnostic oligonucleotides and for gene therapy.
XX CC Antibodies against (I) and (II) are useful for diagnosis and optionally
XX when coupled to therapeutic agents, toxins or other antibodies, to
XX modulate immune and inflammatory responses for example immunological
XX defects such as inflammation, infection, autoimmune diseases, allergy,
XX tumors, leukemia and lymphoma. This sequence represents the murine EDG6
XX protein described in the method of the invention.
XX SQ Sequence 386 AA;
Query Match 82.6%; Score 1623; DB 21; Length 386;
Best Local Similarity 82.8%; Pred. No. 8.6e-169;
Matches 314; Conservative 28; Mismatches 35; Indels 2; Gaps 2;
QY 6 TPVAPESSQQLAAGSHSLIVLHNHSGRLAGRGPEP-GGLALRGLSVAASCLVVLN 64
DB 8 TLVTPESCHRLAASGSHSLIVLHNHSGRLASRGSEDEGGLGMIRGPSVAAGCLVVLN 67
QY 65 LVLVAITSHMRSRRWYVCLVNTLSDLTGAAYLVANVLISGARTFRLAPAOEFLREG 124
DB 68 AMVLAIAIVYRSRRWYVCLVNTLSDLTGLAVYVNVLSGRTTQPSVHFELEGL 127
QY 125 LFTALASTFSLFTAGGERATWVRPAESGATTSRYGFTIGLCWLLAALGLMPLIGW 184
DB 128 LFMALASTFSLFTAGGERATWVR-VAESGATTSRYGFTIGLCWLLAALIGLPLIGW 186
QY 185 NCLCAFQDCSSLLPLYSKRYITLFCVLVFAVGLATIMGLYGAIFRLVQASQKAPRPAR 244
DB 187 NCVCAPFPCSSLLPLYSKRYITLFCVVFVFAVGLATIMGLYGAIFRVVRAVQKSPRPAR 246
QY 245 KARBLTVMILTAFLVCMGPIFGLLLDVFGSNLMAOEYLRGMDDITLAVLANSVNP 304
DB 247 KSRRLMTVMILTAFLVCMGPIFGLLLDVFGSNLMAOEYLRGMDDITLAVFNSHINP 306
QY 305 IIVFSRREVCRAVLSFLCGCCLRLGMRGPGDCLARAVEAHSGASTTDSLSLRPDSFRGS 364
DB 307 LIYSFRSREVCRAVLSFLCGCCLRLGMRGPGDCLARAVEAHSGASTTDSLSLRPDSFRGS 366

QY 365 RSLSFMRREPLSSISSVRS 383
DB 367 RSLSFMRREPLSSISSVRS 385

RESULT 7
AAW80955
ID AAW80955 standard; Protein: 509 AA.
XX AAW80955;
XX AC
XX AA
XX 16-FEB-1999 (first entry)
XX DE
XX Amino acid sequence of an edg-1 receptor.
XX NEHG; edg-1-like receptor; stimulation; cell proliferation; cancer;
XX genetic defect; sickle cell anaemia; agonist; antagonist; antibody;
XX probe.
XX Homo sapiens.
XX OS

Key location/Qualifiers
FH Misc-difference 20
FT /note= "encoded by NGG"
FT Misc-difference 26
FT /note= "encoded by GNT"
XX PN
XX MO9848016-A1.
XX PD
XX 29-OCT-1998.
XX PF
XX 17-APR-1998; 98WO-US07830.
XX PR
XX 24-APR-1997; 97US-0845566.
XX PA
XX (INCYT-) INCYTE PHARM INC.
XX PI
XX Au-Young J, Guegler KJ;
XX WPI: 1998-609989/51.
XX DR N-PSDB; AAW68602.
XX SQ

Claim 1; Fig 1A-1E; p 63pp; English.
PS This is the amino acid sequence of an edg-1-like receptor (NEHG), used
XX in the method of the invention. NEHG can be used to stimulate cell
XX proliferation, especially by expressing encoding polynucleotides,
XX either in vivo (e.g. to promote cell regeneration/differentiation) or
XX in vitro (e.g. to stimulate cell proliferation for transplantation).
XX Such administration may be useful therapeutically, e.g. to stimulate
XX proliferation of cells selected for their ability to fight an
XX infection or a cancer, or correct a genetic defect, e.g. sickle cell
XX anaemia. It can be used to screen for agonists (useful to
XX treat/prevent disorders of abnormal cell growth and differentiation
XX as above) and antagonists, and to generate antibodies. The antagonists
XX can be combined with a suitable carrier in pharmaceutical compositions,
XX useful to treat/prevent disorders of excessive cell proliferation,
XX especially cancers. The NEHG-specific antibodies may be used directly
XX as antagonists, or indirectly as a targeting or delivery mechanism
XX to bring pharmaceutical agents to NEHG-expressing cells. They are
XX also useful to diagnose conditions or diseases characterised by NEHG
XX expression, and to monitor therapeutic interventions. They are useful
XX to produce antisense sequences for therapeutic administration to
XX modulate/prevent NEHG expression. They may also be used to produce
XX probes useful to detect related sequences, or for gene mapping.
XX SQ

Query Match 73.1%; Score 1437; DB 19; Length 509;

Best Local Similarity 76.3%; Pred. No. 2.9e-148;
Matches 303; Conservative 8; Mismatches 42; Indels 44; Gaps 6;

```

OY 1 MNATGTPVAPBSCQQLAAGHSRLIVLHYNSGRLAGRGSPEDGGLRLGLSTVAASCLV 60
DB 1 MNATGTPVAPBSCQQLAAGHSRLIXLHYNSGRLAGRGSPEDGGLRLGLSTVAASCLV 60
OY 61 VLENILVLAATSHMRSRMWVYVCLVNTITSDLLTGAAVLAVLLSGARTFRLAPAOQWFL 120
DB 61 VLENILVLAATSHMRSRMWVYVCLVNTITSDLLTGAAVLAVLLSGARTFRLAPAOQWFL 120
OY 121 REGILFTALAASTFSLFTAGRPFATWVRPVAESGATKTSRYVGTGICWMLAALGLMLP 180
DB 121 REGILFTALAASTFSLFTAGRPFATWVRPVAESGATKTSRYVGTGICWMLAALGLMLP 180
OY 181 ILGNMCCAPDRCSLLPLXSKRYTLFCLVTFPAGYLATIMGXGAIFRLVQASQKAPRP 240
DB 181 ILGNMCCAPDRCSLLPLXSKRYTLFCLVTFPAGYLATIMGXGAIFRLVQASQKAPRP 240
OY 241 AARRKARRLKTYVLMILAFVYCGPRLFGILLADVPSSNMAQ----- 283
DB 241 AARRKARRLKTYVLMILAFVYCGPRLFGILLADVPSSNMAQ----- 283
OY 284 -EYLNGMDWILAVLNSAVNPITYSPRSREVCRAVLSFLCCGCLRLGMRGPDCCLARAV 342
DB 297 RPOLGQOPHNLLPPOGGVQS-----RAOPSSAAGVSGWAC-----EGPDCCLARAV 343
OY 343 EAHSGASTDSSLRPDRSFRGSRSLSPFRMRPLSSIS 379
DB 344 EAHSGA-----SNHROLSEAKGOLS-----RLPLAQLS 371

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RESULT 8

AA081577
ID AA081577 standard; Protein; 276 AA.

AC AA081577;

DE 22-FEB-1999 (first entry)

XX EDG-1-like G-protein coupled receptor polypeptide.

XX EBY-induced G-protein coupled receptor; EBI-2; Epstein-Barr Virus; ulcer;
XX endothelium-differentiation gene; EDG-1-like G-protein coupled receptor;
XX recombinant; agonist; asthma; Parkinson's disease; heart failure; asthma;
XX hypertension; urinary retention; osteoporosis; antagonsist; hypertension;
XX angina pectoris; myocardial infarction; allergy; psychosis; depression;
XX migraine; vomiting; stroke; eating disorder; migraine headache; cancer;
XX prostatic hypertrophy; detection; drug screening.

OS Homo sapiens.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Peptide 1..16

XX Protein /note="signal peptide" 17..276

XX Misc-difference 207 /note="mature protein"

XX Misc-difference 218 /note="encoded by GAC"

XX Misc-difference 220 /note="encoded by AAG"

XX Misc-difference 220 /note="encoded by TAC"

XX MO09850549-A2.

XX 12-NOV-1998.

XX 07-MAY-1998; 98WO-0509048.

XX 07-MAY-1997; 97US-0852824.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Li Y, Ruben SM;

XX WPI: 1999-034722/03.

XX N-PSDB: AAV69761.

XX New isolated human G-protein coupled receptors - used to develop
XX products for treating e.g. asthma, Parkinson's disease, heart
XX failure, osteoporosis, hypertension, psychoses, eating disorders or
XX cancers

XX Claim 1; Fig 3A-B; 65bp; English.

XX This represents a EDG-1-like G-protein coupled receptor polypeptide.
XX The encoding DNA is deposited under the accession number ATCC No:
XX 209004. The invention provides two human G-protein coupled receptor
XX polypeptides. The polypeptides are human Epstein-Barr Virus (EBV)-induced
XX G-protein coupled receptor, designated EBI-2 polypeptide and a human
XX endothelium-differentiation gene (EDG) like G-protein coupled receptor,
XX designated EDG-1-like G-protein coupled receptor. Vectors comprising the
XX host cells for the recombinant production of the proteins. Agonists for
XX G-protein coupled receptors can be used for the treatment of asthma,
XX Parkinson's disease, acute heart failure, hypertension, urinary retention
XX and osteoporosis. Antagonists can be used for the treatment of
XX hypertension, angina pectoris, myocardial infarction, ulcers, asthma,
XX allergies, psychoses, depression, migraine, vomiting, stroke, eating
XX disorders, migraine headaches, cancer and benign prostatic hypertrophy.
XX The products can also be used for detection, diagnosis and drug
XX screening.

XX Sequence 276 AA:

XX Query Match 65.2%; Score 1281; DB 20; Length 276;

XX Best Local Similarity 97.3%; Pred. No. 1.5e-131;
XX Matches 252; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

OY 1 MNATGTPVAPBSCQQLAAGHSRLIVLHYNSGRLAGRGSPEDGGLRLGLSTVAASCLV 60

DB 17 MNATGTPVAPBSCQQLAAGHSRLIVLHYNSGRLAGRGSPEDGGLRLGLSTVAASCLV 76

OY 61 VLENILVLAATSHMRSRMWVYVCLVNTITSDLLTGAAVLAVLLSGARTFRLAPAOQWFL 120

DB 77 VLENILVLAATSHMRSRMWVYVCLVNTITSDLLTGAAVLAVLLSGARTFRLAPAOQWFL 136

OY 121 REGILFTALAASTFSLFTAGRPFATWVRPVAESGATKTSRYVGTGICWMLAALGLMLP 180

DB 137 REGILFTALAASTFSLFTAGRPFATWVRPVAESGATKTSRYVGTGICWMLAALGLMLP 196

OY 181 ILGNMCCAPDRCSLLPLXSKRYTLFCLVTFPAGYLATIMGXGAIFRLVQASQKAPRP 240

DB 197 ILGNMCCAPDRCSLLPLXSKRYTLFCLVTFPAGYLATIMGXGAIFRLVQASQKAPRP 256

OY 241 AARRKARRLKTYVLMILAFVYCGPRLFGILLADVPSSNMAQ----- 283

DB 257 AARRKARRLKTYVLMILAFVYCGPRLFGILLADVPSSNMAQ----- 283

OY 241 AARRKARRLKTYVLMILAFVYCGPRLFGILLADVPSSNMAQ----- 283

DB 257 AARRKARRLKTYVLMILAFVYCGPRLFGILLADVPSSNMAQ----- 283

OY 241 AARRKARRLKTYVLMILAFVYCGPRLFGILLADVPSSNMAQ----- 283

DB 257 AARRKARRLKTYVLMILAFVYCGPRLFGILLADVPSSNMAQ----- 283

OY 241 AARRKARRLKTYVLMILAFVYCGPRLFGILLADVPSSNMAQ----- 283

DB 257 AARRKARRLKTYVLMILAFVYCGPRLFGILLADVPSSNMAQ----- 283

OY 241 AARRKARRLKTYVLMILAFVYCGPRLFGILLADVPSSNMAQ----- 283

DB 257 AARRKARRLKTYVLMILAFVYCGPRLFGILLADVPSSNMAQ----- 283

OY 241 AARRKARRLKTYVLMILAFVYCGPRLFGILLADVPSSNMAQ----- 283

DB 257 AARRKARRLKTYVLMILAFVYCGPRLFGILLADVPSSNMAQ----- 283

OY 241 AARRKARRLKTYVLMILAFVYCGPRLFGILLADVPSSNMAQ----- 283

DB 257 AARRKARRLKTYVLMILAFVYCGPRLFGILLADVPSSNMAQ----- 283

OY 241 AARRKARRLKTYVLMILAFVYCGPRLFGILLADVPSSNMAQ----- 283

DB 257 AARRKARRLKTYVLMILAFVYCGPRLFGILLADVPSSNMAQ----- 283


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XX Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;
KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
KW diagnostics; forensic test; gene mapping; genetic disorder;
XX biodiversity; gene therapy; nutrition.
OS Homo sapiens.
XX MO200154477-A2.
XX 02-AUG-2001.
XX 25-JAN-2001; 2001MO-US02687.
XX 25-JAN-2000; 2000US-0491404.
PR 17-JUL-2000; 2000US-0617746.
PR 03-AUG-2000; 2000US-0631451.
PR 15-SEP-2000; 2000US-0663870.
XX (HYSE-) HYSEQ INC.
XX Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi Y,
PI Cao Y, Drmanac RA, Zhang J, Werhman T;
XX WPI: 2001-476164/51.
DR N-PSDB; AAH98657.
XX Isolated polypeptide for treatment of diseases, diagnostics, raising
PT antibodies and research use -
XX Claim 20; Page 1051; 1275pp; English.
XX The present invention provides the protein and coding sequences of novel
CC proteins from a variety of organisms, including human, dog, cat, horse,
CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
CC urchin and tomato. These were derived from expressed sequence tags (ESTs)
CC from the organism of interest. They can be used in diagnostics,
CC forensics, gene mapping, identification of mutations, to assess
CC biodiversity and for nutritional purposes. The present sequence is a
CC protein of the invention.
XX Sequence 130 AA:
SQ
Query Match 34.1%; Score 671; DB 22; Length 130;
Best Local Similarity 100.0%; Pred. No. 3.2e-65;
Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 255 MILAFLVCMGPIFGILLADVFGSNLMAOEYLRGMDMILAVLNSAVNPITYSFRSREV 314
DB 1 MILAFLVCMGPIFGILLADVFGSNLMAOEYLRGMDMILAVLNSAVNPITYSFRSREV 60
QY 315 CRAVLSTCCGCLRLGMRGDCCLARAVEAHSASTTDSLSLRDSFRSRSLSFMRREP 374
DB 61 CRAVLSTCCGCLRLGMRGDCCLARAVEAHSASTTDSLSLRDSFRSRSLSFMRREP 120
QY 375 LSSISVSRSI 384
DB 121 LSSISVSRSI 130
RESULT 12
AAW01664
ID AAW01664 standard; Protein; 383 AA.
XX AAW01664;
AC
XX 01-APR-1997 (first entry)
XX p(rat-edg), G-protein coupled receptor.
DE
XX p(rat-edg), G-protein coupled receptor.
KW p(H218); G-protein coupled receptor; cell differentiation; proliferation;
KW proline directed kinase; cell division; growth factor response; rat-edg;
KW therapy; diagnosis.
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XX Ratius ratius.
XX OS
XX US5585476-A.
XX 17-DEC-1996.
XX 15-FEB-1994; 94US-0196989.
XX 15-FEB-1994; 94US-0196989.
XX (MACL/) MACLENNAN A J.
XX Macleennan AJ;
PI
XX WPI: 1997-051235/05.
DR N-PSDB; AAT58506.
XX DNA encoding rat protein p(H218) - associated with cell
PT proliferation and/or differentiation
XX Example 9; Column 17-20; 33pp; English.
XX This sequence is a novel rat protein p(rat-edg), a member of the
CC G-protein coupled receptor (GPR) superfamily of proteins. The
CC amino acid similarity between p(H218) (AAW01663) and p(rat-edg) suggests
CC that they may be activated by the same endogenous ligand(s). The
CC expression pattern of mRNA transcripts of both genes in cell lines,
CC various rat tissues and developing rat brain suggests that they both
CC play a role in cell proliferation and/or differentiation.
XX Sequence 383 AA:
SQ
Query Match 33.9%; Score 666; DB 18; Length 383;
Best Local Similarity 40.0%; Pred. No. 4.9e-64;
Matches 150; Conservative 69; Mismatches 126; Indels 30; Gaps 8;
QY 1 MNATGPAPAPSCCOOLAAGSHRLVLVHNHSGRLAGRGDEDEGLALRGLSYAASCLV 60
DB 2 VSTSIPIYVKALRGVSDYGNVDIIVRYNTGKL-NIGVEKDHGIKLTSVFILICCLI 60
QY 61 VLENLLVAITSHMSRRWYVCIVNTTSDLLTGAAYLANVLGARTPRLPAPQWFL 120
DB 61 ILENFVLLTITWKTKFHRPMYFIGNLALSDLAGAVATANLLSGATYTKLPAPQWFL 120
QY 121 REGLLFTALASTPSLFTTAGERFATMWRPVAEGATTSVYFGICWMLTALLGMLP 180
DB 121 REGSMFVALSASFLLAIAIERITYTLMKMLHNG-SNRSRSLISACWYSLILGGLP 179
QY 181 ILGNMCLAFDRCSLLPLYSKRYLLFCLVTFAGVATIMGLYGAIFRLVQASQ----- 235
DB 180 IMGWNCISSLSGCSVLPDLHKHYLLFCTYFTLLLSIVLYCRISVLTFRSRLTFR 239
QY 236 ----KAPPARARRKRLIKTYLMTLLAFVLCWGPFLGLLADYFGSNLMAOEYLRGMDW 291
DB 240 KNISKASR--SSEKSLALIKTVIIVLSVFIACWMPFLTLLLDV-GCKAKTCDILYAEY 296
QY 292 ILALAVNSAVNPITYSFRSREVCRVAVLSPL-CCGCLRLGMRG-----PGDCIARAVE 343
DB 297 FLVLAVLNSGTPILITYTLTNKEMRRAFIRIISCCCPNGDSAGKFRKPIIFGMEFSR--- 353
QY 344 AHSASTTDSLSLRPR 358
DB 354 -----SKSDNSSHPQ 363
RESULT 13
AAW87791
ID AAW87791 standard; Protein; 383 AA.
XX AAW87791;
AC
XX 12-MAR-1999 (first entry)
XX
```


OY 181 LIGNCCAFEDRCSSLPYKRYILFCVIFAGVLATIMGLYGAIFRLVQASGQ----- 235
 DB 179 IMGNNCISLSSGCTVPLVHKHILFCTVIFLLLSITVILXCRISLVIRSRRLTR 238
 OY 236 ----KAPPAARRAKRLTVMILIAFLVCGPPLFGILLADVFSGNMAOETLRGMD 291
 DB 239 KNISKASR--SSEKSLALKTIVIVLVSFTACWAPLFLILLDV--GCKAKTCIDILYKAY 295
 OY 292 ILALAVINSAVNPITYFSRSEVCRAVLSFL--CCGCLRLGMRG-----PGDCLARAWE 343
 DB 296 FLVLAIVNSGNPIITVITLTKEMKRAIRIVSCCKPCPDGSDAKFKRPILIPGMEFSR--- 352
 OY 344 AHSQASTDSSLRP 358
 DB 353 -----SKSDNSSHPQ 362

RESULT 15

AA71305
 ID AA71305 standard; Protein; 500 AA.

XX
 AC AA71305;

DT 02-NOV-2000 (first entry)

DE Human orphan G protein-coupled receptor hCHN6.

KW Human; orphan G protein-coupled receptor; GPCR; hCHN6; drug screening;
 transmembrane receptor; expressed sequence tag; EST; signal cascade.

XX Homo sapiens.

OS
 PN WO200031258-A2.

XX 02-JUN-2000.

PF 13-OCT-1999; 99WO-US23687.

XX 20-NOV-1998; 98US-0109213.
 PR 16-FEB-1999; 99US-0120416.
 PR 26-FEB-1999; 99US-0121852.
 PR 12-MAR-1999; 99US-0123946.
 PR 12-MAR-1999; 99US-0123949.
 PR 28-MAY-1999; 99US-0136436.
 PR 28-MAY-1999; 99US-0136437.
 PR 28-MAY-1999; 99US-0136439.
 PR 28-MAY-1999; 99US-0136567.
 PR 28-MAY-1999; 99US-0137127.
 PR 28-MAY-1999; 99US-0137131.
 PR 29-JUN-1999; 99US-0141448.
 PR 29-SEP-1999; 99US-0156555.
 PR 29-SEP-1999; 99US-0156633.
 PR 29-SEP-1999; 99US-0156634.
 PR 29-SEP-1999; 99US-0156653.
 PR 01-OCT-1999; 99US-0157280.
 PR 01-OCT-1999; 99US-0157281.
 PR 01-OCT-1999; 99US-0157282.
 PR 01-OCT-1999; 99US-0157293.
 PR 01-OCT-1999; 99US-0157294.
 PR 12-OCT-1999; 99US-0416760.
 PR 12-OCT-1999; 99US-0417044.

XX (AREN-) ARENA PHARM INC.

XX Chen R, Dang HT, Liaw CW, Lin I;

XX WPI; 2000-400068/34.

XX N-PSDB; AAD01132.

XX Novel human orphan G protein-coupled receptors and the encoding cDNAs
 PT for use in the identification of G protein-coupled receptor agonists -
 XX

PS Claim 58; Page 79-81; 102pp; English.

XX The present amino acid sequence is the hCHN6, an endogenous human
 CC orphan G protein-coupled receptor (GPCR). The hCHN6 cDNA was identified
 CC using ESTs (expressed sequence tag) A804531 and 2134670 as a probe.
 CC The orphan GPCR of the invention, like all GPCRs has seven transmembrane
 CC alpha helices with an extracellular N-terminus and an intracellular
 CC C-terminus. However, no endogenous ligands has yet been identified for
 CC the proteins of the invention. The orphan GPCRs may be used in the
 CC identification of their endogenous ligands, and to screen potential GPCR
 CC agonists and antagonists for use as pharmaceutical agents. The proteins
 CC may also be used in the study of GPCR-mediated signalling cascades, and
 CC to elucidate their precise role in normal and diseased human conditions.
 CC Nucleic acid encoding human orphan GPCRs may be used for tissue
 CC localisation expression analysis to provide information about their
 CC function in healthy and pathological states.

SO Sequence 500 AA:

Query Match 32.9%; Score 647.5; DB 21; Length 500;
 Best local similarity 40.8%; Pred. No. 7,5e-62;
 Matches 154; Conservative 50; Mismatches 126; Indels 47; Gaps 7;

OY 22 SRLVLYHNHSGRLAGSGPEDGIGALRGSLVAASCIWLENTLYLAITSHMSRMV 81
 DB 114 SEVIVLHYNTIGKLRGASTOPGAGLRADAVCYLAVCFYLENAVLLVLRHPRFHAP 173
 OY 82 YYCLVNTITLSDLTGAAYLANVLLSGARFRLAPACQFLREGILFTALASTFSLFTAG 141
 DB 174 FLIGSLITLSDLLAGAAVYANILSLPLTKLSPALMFARREGVFAVLAASVLSLAL 233
 OY 142 ERFATMVR---PVAESGATKTSRVYGFIGLCVLLAAILGMLPLIGMNCICAFDCCSLL 197
 DB 234 ERSILTMARCGPAPVSSRG-----RTLMAAAAGVSLILGLPLALGWNCLGRDCKSTYL 288
 OY 198 PLYSKRYILFCVIFAGVLATIMGLYGAIFRLVQASGQAR-RPA-----ARRKAR- 247
 DB 289 PLYKAYVLFVCLAFVGIILALCALYARIYCYRANARRLPARPAGTSTRARRKPRS 348
 OY 248 -RLTKYVIMILIAFLVCGPPLFGILLADVFSGNMAOETLRGMDITLALAVNSAVNPIT 306
 DB 349 IALRTLSVVLAFVACWGPPLFLILLDVACPARTCPVLLDA-DPLGLAMANSILNPIIT 407
 OY 307 YSFRSEVRCRAVLSFLCCG-----CLRIGMRGPDCIAR 340
 DB 408 YTLFRDILRHALLRLVCCGRHSCGRDPSGSQSASAAEASGILRCLPPGLDGSPSGSER 467
 OY 341 AVEAHSQASTDSSLRP 357
 DB 468 SSPQRDGLDTSSTGSP 484

Search completed: December 9, 2002, 12:04:10
 Job time : 40 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 9, 2002, 12:03:07 : Search time 35 Seconds
(Without alignments)
2260.631 Million cell updates/sec

Title: US-09-786-926-1
Perfect score: 1966
Sequence: 1 MNATGVPVAPESQQLAAG.....RSLSPFMRPELSSISVRSI 384

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPREMBL_21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1966	100.0	384	4 095977	095977 homo sapien
2	1623	82.6	386	11 092011	092011 mus musculu
3	655.5	33.3	362	13 09DDK4	09ddk4 brachydanio
4	653	33.2	382	11 09DC35	09dc35 mus musculu
5	649	33.0	382	11 09R235	09r235 mus musculu
6	645.5	32.8	398	4 09H228	09h228 homo sapien
7	643.5	32.7	378	11 09Z009	09z009 mus musculu
8	640	32.6	384	13 09PU08	09pu08 fugu rubrip
9	638	32.5	400	11 09UKM5	09ukm5 rattus norv
10	636	32.3	400	11 09IX56	09ix56 mus musculu
11	635.5	32.3	382	4 09ANY8	09any8 homo sapien
12	632	32.1	387	11 099NM8	099nm8 mus musculu
13	628	31.9	400	11 09QY79	09qy79 rattus norv
14	618	31.4	326	11 099NR2	099nr2 dipodomys h
15	614	31.2	326	11 099NR4	099nr4 hystrix bra
16	613.5	31.2	326	11 099NR1	099nr1 heteroceph

17	613	31.2	326	6 09BF63	09bf63 ochotona hy
18	612.5	31.2	326	11 099NR5	099nr5 mus musculu
19	612.5	31.2	326	11 099NR3	099nr3 erehizon d
20	611.5	31.1	326	6 09BF60	09bf60 lemur calta
21	610.5	31.1	326	11 099NR0	099nr0 cavia tachu
22	610	31.0	326	6 09BF73	09bf73 condylura c
23	609	31.0	326	6 09BF66	09bf66 elephantu
24	609	31.0	326	11 099NR7	099nr7 agouti lacz
25	608	30.9	326	6 09BF70	09bf70 trichechus
26	608	30.9	326	6 09BF57	09bf57 hylobates c
27	608	30.9	326	6 09BF49	09bf49 tiragelaphus
28	608	30.9	326	6 09BF48	09bf48 sus scrofa
29	608	30.9	326	6 09BF47	09bf47 okapia john
30	607.5	30.9	326	11 099NR9	099nr9 hydrochoeru
31	607	30.9	326	6 09BF58	09bf58 macaca mula
32	607	30.9	326	11 099NR8	099nr8 castor cana
33	606.5	30.8	326	6 09BF53	09bf53 rousettus l
34	606	30.8	325	11 099NR9	099nr9 tamias stri
35	606	30.8	326	6 09BF72	09bf72 sorex arane
36	606	30.8	326	6 09BF67	09bf67 macrosellid
37	605	30.8	326	6 09BF68	09bf68 loxodonta a
38	605	30.8	326	6 09BF46	09bf46 equus cabal
39	604	30.7	326	6 09BF75	09bf75 myrmecophag
40	604	30.7	326	6 09BF74	09bf74 erinaceus c
41	604	30.7	326	6 09BF69	09bf69 procavia ca
42	604	30.7	326	6 09BF52	09bf52 megaptera n
43	604	30.7	326	6 09BF45	09bf45 ceratotheri
44	602.5	30.6	326	11 099NR8	099nr8 myocastor c
45	602	30.6	326	11 099NR7	099nr7 muscardinus

ALIGNMENTS

RESULT 1					
ID	095977	PRELIMINARY:	PRT:	384	AA.
AC	095977;				
DT	01-MAY-1999 (TREMBLrel. 10, Created)				
DT	01-MAY-1999 (TREMBLrel. 10, Last sequence update)				
DT	01-MAR-2002 (TREMBLrel. 20, Last annotation update)				
DE	Putative G-protein coupled receptor, EDG6 precursor (Hypothetical 41.6 kDa protein).				
DE					
GN	EDG6				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TaxID=9606;				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=99009331; PubMed=9790765;				
RA	Graefer M.H., Bernhard G., Lipp M.;				
RT	*EDG6, a novel G protein-coupled receptor related to receptors for bioactive lysophospholipids, is specifically expressed in lymphoid tissue.";				
RT					
RL	Genomics 53:164-169(1998).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=BLOOD;				
RA	Strausberg R.;				
RL	Submitted (OC2-2001) to the EMBL/Genbank/DBJ databases.				
DR	EMBL: AJ000479; CA04118.1; -				
DR	EMBL: BC014970; AAH14970.1; -				
DR	InterPro: IPR004064; EDG6receptor.				
DR	InterPro: IPR000276; GPCR_Rhodospn.				
DR	Pfam: PF00001; 7tm_1; 1.				
DR	PRINTS: PR01526; EDG6RECEPTOR.				
DR	PRINTS: PR00237; GPCR_RHODOPSIN.				
DR	PRINTS: PR01523; SLPRECEPTOR.				
DR	PROSITE: PS50262; G_PROTEIN_RECPT_F1_2; 1.				
DR	G-protein coupled receptor; Hypothetical protein; Receptor; signal.				
KW	SIGNAL				
FT					

SEQUENCE 384 AA: 41623 MW: 369A7BC56AB46A47 CRC64;
Query Match 100.0%; Score 1966; DB 4; Length 384;
Best Local Similarity 100.0%; Pred. No. 4,7e-151;
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNTGTPVAPESCOOLAAGHSHRLVLYHNHSGRLAGRGPEDEGLGALRGLSVAASCLV 60
DB 1 MNTGTPVAPESCOOLAAGHSHRLVLYHNHSGRLAGRGPEDEGLGALRGLSVAASCLV 60
QY 61 VLENLLVLAITSHMRSRRMYVYCLVNTLSDLLTGAAYLANVLLSGARTFRLAPAQWFL 120
DB 61 VLENLLVLAITSHMRSRRMYVYCLVNTLSDLLTGAAYLANVLLSGARTFRLAPAQWFL 120
QY 121 REELLETTALAASFSLFTFAGERFATWVRPAVESGATKTSRYVGFGLCWLIALGLMP 180
DB 121 REELLETTALAASFSLFTFAGERFATWVRPAVESGATKTSRYVGFGLCWLIALGLMP 180
QY 181 LIGMNCICAFDRCSLLPLYSKRYILFCLVIFAGVLATIMGLYGAIFRLVQASGOKAPRP 240
DB 181 LIGMNCICAFDRCSLLPLYSKRYILFCLVIFAGVLATIMGLYGAIFRLVQASGOKAPRP 240
QY 241 AARRKARLLKTYLMLLAFVYCWGPLEGLLADYFGSNLMAOEYLRGMDWILALAVLNS 300
DB 241 AARRKARLLKTYLMLLAFVYCWGPLEGLLADYFGSNLMAOEYLRGMDWILALAVLNS 300
QY 301 AVNPITTSFRRSREVCRAVLSFLCCGCLRLGMRGPDCLARAVEAHSGASTDSSLRPRS 360
DB 301 AVNPITTSFRRSREVCRAVLSFLCCGCLRLGMRGPDCLARAVEAHSGASTDSSLRPRS 360
QY 361 FRGSRSLSFRRMRREPLSSISVSRSI 384
DB 361 FRGSRSLSFRRMRREPLSSISVSRSI 384

RESULT 2
Q920L1 PRELIMINARY; PRT; 386 AA.
ID Q920L1
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE G protein-coupled receptor precursor.
GN EDG6 OR EDG6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C; TISSUE=FETAL SKIN-DERIVED;
RX MEDLINE=99009311; PubMed=9790765;
RA Graeler M.H., Bernhardt G., Lipp M.;
RT "EDG6, a novel G protein-coupled receptor related to receptors for
RT bioactive lysophospholipids, is specifically expressed in lymphoid
RT tissue";
RL Genomics 53:164-169(1998).
DR EMBL: AJ006074; CA06847.1; -.
DR MGD: MGI:1333809; Edg6.
DR InterPro: IPR004064; EDG6receptor.
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm.1; 1.
DR PRINTS: PRO1526; EDG6RECEPTOR.
DR PRINTS: PRO0237; GPCR_RHODOPSIN.
DR PRINTS: PRO1523; S1PRECEPTOR.
DR PROSITE: PS50262; G_PROTEIN_RECPEP_FL_2; 1.
KW Receptor; Signal.
FT SIGNAL 1 37 POTENTIAL.
FT CHAIN 38 386 G PROTEIN-COUPLED RECEPTOR EDG6.
SQ SEQUENCE 386 AA: 42262 MW: 8AB32CB602BA922 CRC64;

Query Match 82.6%; Score 1623; DB 11; Length 386;

Best Local Similarity 82.8%; Pred. No. 2.5e-123;
Matches 314; Conservative 28; Mismatches 35; Indels 2; Gaps 2;

QY 6 TPVAPESCOOLAAGHSHRLVLYHNHSGRLAGRGPEDEGLGALRGLSVAASCLVLEN 64
DB 8 TLVTPESCHRLAAGSHSLVLYHNHSGRLARSGSDGGGLGMRGPVAAACLVLEN 67
QY 65 LLYVAITSHMRSRRMYVYCLVNTLSDLLTGAAYLANVLLSGARTFRLAPAQWFLREG 124
DB 68 AMVLAIAITMRSRRMYVYCLVNTLSDLLTGLAYVNVLLSGRTTQLSPVMFLREG 127
QY 125 LFTALAASFSLFTFAGERFATWVRPAVESGATKTSRYVGFGLCWLIALGLPILGW 184
DB 128 LFMALAASFSLFTFAGERFATWVR-VAESGATKTSRYVGCICGLWLLAILGLPILGW 186
QY 185 NCLCAFDRCSLLPLYSKRYILFCLVIFAGVLATIMGLYGAIFRLVQASGOKAPRAPAR 244
DB 187 NCVCAPFRCSLLPLYSKRYILFCLVIFAGVLATIMGLYGAIFRLVQASGOKAPRAPAR 246
QY 245 KARRLKTYLMLLAFVYCWGPLEGLLADYFGSNLMAOEYLRGMDWILALAVLSAVNP 304
DB 247 KSRRLNTVLMILVAFVYCWGPLEGLLADYFGSNVMAOEYLRGMDWILALAVNSAINP 306
QY 305 ILYSFRSREVCRAVLSFLCCGCLRLGMRGPDCLARAVEAHSGASTDSSLRPRDSFGS 364
DB 307 LIYSFRSREVCRAVLAFLCCGCLRLGMRGPDCLARAVEAHSGASTDSSLRPRDSFRTS 366
QY 365 RSLSFRRMRREPLSSISVSRS 383
DB 367 RSLSFRRMRREPLSSISVSRS 385

RESULT 3
Q9DDK4 PRELIMINARY; PRT; 362 AA.
ID Q9DDK4
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Sphingosine 1-phosphate receptor.
GN EDG1.
OS Brachydanio rerio (Zebrafish) (zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=20563813; PubMed=11112429;
RA Im D.S., Ungar A.R., Lynch K.R.;
RT "Characterization of a zebrafish (Danio rerio) sphingosine 1-phosphate
RT receptor expressed in the embryonic brain";
RL Biochem. Biophys. Res. Commun. 279:139-143(2000).
DR EMBL: AF31294; AAG3430.1; -.
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm.1; 1.
DR PRINTS: PRO0237; GPCR_RHODOPSIN.
DR PROSITE: PS00237; G_PROTEIN_RECPEP_FL_1; UNKNOWN_1.
DR PROSITE: PS50262; G_PROTEIN_RECPEP_FL_2; 1.
KW Receptor.
SQ SEQUENCE 362 AA: 40583 MW: 43A398871DA2D9D4 CRC64;

Query Match 33.3%; Score 655.5; DB 13; Length 362;
Best Local Similarity 41.0%; Pred. No. 3.6e-45;
Matches 152; Conservative 56; Mismatches 136; Indels 25; Gaps 9;

QY 24 LIVLYHNHSGRLAGRGPEDEGLGALRGLSVAASCLVLENLLVLAITSHMRSRRMYV 83
DB 4 LIARIYNTGKF--RKVHKDGLKADSVVFTIYCCFIILENVLLIIMRTKFKHKPMY 61
QY 84 CLVNTTSLDITLGAAYLANVLLSGARTFRLAPAQWFLREGILLFALAASFSLFTGER 143
DB 62 FIGNIALSDLAGVYVYNTANILLSGANTYKLTPTQWFRREGSMFVALAASFSLAIATER 121


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OY 121 REGLEFALTALSTPELTAEGERATWVRPAESGAKRTSRVYFETGLCWHLAALLGMP 160
Db 120 REGSMFVALSASVSTBLAIATERITMLKMLHNG-SNSSSFLLISACWVILSLTGLP 178
OY 181 LIGMNCALCFRCSSLLPLYSKRYILFCLVYFAGVLATIMGLYGAIFRLVOASQO----- 235
Db 179 SMGNWCIJSLSCSGSTVLEPLYKHRYILFCTVFTLLLSIYLICRISLVLRITSRLRTER 238
OY 236 ----KAPPARRRKARILKTVMLLILAFVCMQPIFEGLLIADYFGSNLMAOEYLKGMW 291
Db 239 KNISKAASR--SSEKSLALCKTVIIVLSVFACVAMPLEIILLLDV-GCKAKTCDILYKAEY 295
OY 292 ILALAVLNSAANPIIYFSRREVCRAVLSEF-CGCGJRLTMRG-----PGDCLARAVE 343
Db 296 FLVLAVLNSGTNPILITLTLENEMRAPRIIYVSCCKCNGDPSACKFRKPIIPGMEFSR--- 352
OY 344 AHSGASTDSSLRPR 358
Db 353 -----SKSDNSSHPO 362

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RESULT 6
09H228 PRELIMINARY; PRT; 398 AA.
ID 09H228
AC 09H228;
DT 01-MAR-2001 (TREMBLrel, 16, Created)
DR 01-MAR-2001 (TREMBLrel, 16, Last sequence update)
DE 01-JUN-2002 (TREMBLrel, 21, Last annotation update)
DE Sphingosine 1-phosphate receptor Edg-8 (SPPR) (putative G-protein
DE coupled receptor).
DE GPCR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RN SEQUENCE FROM N.A.
RA Im D., Lynch K.R.;
RT "Characterization of a human sphingosine 1-phosphate receptor, Edg-
RT 8."
RN [2]
RN Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
RP SEQUENCE FROM N.A.
RA Kochevali R., Loughran T.P. Jr.;
RT "Characterization of a novel human gene (hsppr) with homology to rat
RT sphingosine 1-phosphate receptor and differential expression in LGL
RT leukemia patients";
RN [3]
RN Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RN SEQUENCE FROM N.A.
RA Takeda S., Kadowaki S., Haga T., Takeasu H., Mitaku S.;
RT "Identification of G protein-coupled receptor genes from the human
RT genome sequence.";
RN [4]
RN Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF317676; AAC38113.1; -
DR EMBL; AF331840; AAU57041.1; -
DR EMBL; AB083602; BAB89315.1; -
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR01561; BDG8RECEPTOR.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G-PROTEIN_RECP_F1_1; UNKNOWN_1.
DR PROSITE; PS50262; G-PROTEIN_RECP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 398 AA: 41775 MW; 34ADC6C40D8250BF CRC64;

Query Match 32.8%; Score 645.5; DB 4; Length 398;
Best Local Similarity 40.8%; Pred. No. 2.5e-44;
Matches 154; Conservative 50; Mismatches 126; Indels 47; Gaps
22 SRTLVLYHNSGSLARGPDPDGGALGRLGSVAASCLVYENLLVLAATISHRKSRKV 81
I :|||||:|:| | | | | | | | | | | | | | | | | | | | | | | | | |
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Db      12 SEVIVAHNYTCKLGARYGCGAGLRADAAVVCGLAVCAFIENLAVLLVIGRHHFAPM  71
Qy      82 YVCVYNITLSDLTGAATLVANVLGSGARTFRLAPAQWELREGLLFTLAASTESLFTAG  141
Db      72 FLLISLSDLTDLGAAANAAILLISGLPTLLSPALMFAREGVAFVATASVLSLAIAL  133
Qy      142 ERFATMVR----PVASEATKTSRYGFTIGCLWLLALIGMLPLLGWNCCLACDRCSLL  197
Db      132 EESLTMARGAPAVSSR----KLLMAAAAAMGVSLILGLPLLGWNCCLGRDAGCTVL  186
Qy      198 PLYSKRLLYFLCIVTFAVGLATIMLGIAIFRLVQASOKAP-RA-----ARRAR-  247
Db      187 PLYAAAYVFCVLAIVGLLAICALYARIQVYAAKRRLLPARGDTAGTTSTRARRPRS  246
Qy      248 -RLKTYVLMILLAEVLCWGPLFGLLADVFGSNIWMAQGYLRGMDWILALVLSAAVPII  306
Db      247 IALLTEISVLLAEFAVCAWGPFLFLLLLDVACPARTCVLLQA-DPFLGLMAANSLNPII  305
Qy      307 YSFRREYECRAVLSFLCG-----CLRLMGKPGDCLAR  340
Db      306 YTLNRDRLRAHLRLRYCCGRHSCHGRDPSGSOOSASAAEAGGLRCLPLPGDSSFSGSER  365
Qy      341 AVEAHSASTSDSLRP  357
Db      366 SSPQRDGLDITGSGTSP  382

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RESULT 7			
09Z009			
ID	09Z009	PRELIMINARY;	PRT; 378 AA.
AC	09Z009;		
DT	01-MAY-1999 (TrEMBLrel. 10, Created)		
DT	01-MAY-1999 (TrEMBLrel. 10, Last sequence update)		
DT	01-MAR-2002 (TrEMBLrel. 20, Last annotation update)		
DE	LYSOPHOSPHOLIPID receptor B3.		
CN	LPB3 OR EDG3.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Cranialta; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=129SVJ;		
RX	MEDLINE=99112320; PubMed=9931453;		
RA	Zhang G., Contos J.T.A., Weiner T.A., Fukushima N., Chun J.;		
RT	"Comparative analysis of three murine G-protein coupled receptors		
RT	activated by sphingosine-1-phosphate.";		
RL	Gene 227:89-99(1999).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RA	Ohta K., Wada A., Igarashi Y.;		
RT	"Mus musculus sphingosine 1-phosphate receptor Edg3 gene, complete.";		
RL	Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.		
DR	EMBL: AF1080023; AAD1697.1; -		
DR	EMBL: AB028143; BAA78207.1; -		
DR	MGI: 1339385; Edg3.		
DR	InterPro: IPR00194; ArParse_a/bcentre.		
DR	InterPro: IPR004062; Edg3receptor.		
DR	InterPro: IPR000276; GPCR_Rhodpsn.		
DR	InterPro: IPR004061; s1preceptor.		
DR	Pfam: PF00001; 7tm_1.1		
DR	PRINTS: PRO1524; EDG3RECEPTOR.		
DR	PRINTS: PRO0237; GPCRRHODOPSN.		
DR	PRINTS: PRO1523; S1PRECEPTOR.		
DR	PROSITE: PS00152; ATPASE_ALPHA_BETA; UNKNOWN_1.		
DR	PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.		
DR	PROSITE: PS50262; G_PROTEIN_RECEP_F1_2; 1.		
KW	Receptor.		
SO	SEQUENCE	378 AA;	42270 MW; F46B25E77ECDC8 CRC64;
Query Match		32.7%;	Score 643.5; DB 11; Length 378;
Best local similarity		42.1%;	Pred. NO. 3.5e-44;
Matches 150;	Conservative	62;	Mismatches 125; Indels 19; Gaps

QY	28	HYNSGRLAGR--GGPDSGLGALRGLASVASCIVLENTLVLAATTHMSRRRWYYCYL	86
Db	21	HYDVYKLAGRLRDPDEGGTLITTLTFLVTCSTFYLENLMVLAIAWKNNKHNNRYEPFG	80
QY	87	NTTSLDILTGAAYLANVLISGARTERFLPAQWFLREGLEFLTALAATSTFLTAGERPAT	146
Db	81	NLALCDLLAGLAIKVNIILMSGRKTFESLSPYWFLEGGSMFALGASTCSLLAIAIERHLT	140
QY	147	MVRPYASGATKTSRVYGFGLCWLLAALLGMLPLGNNCLCAEDRCSSLLPLYSKRYIL	206
Db	141	MIR-MRPYDANKKHVFLIIMCWMILASLALPILGNCCLENPFDCSTIILPYSKKYIA	199
QY	207	FCVIFAGVAVLTIMGVCAIFRIYVQASGOKAPRAPARRKARILKTVIMILIAFYICGP	266
Db	200	FLISFTFALIVATYILTKRITCVLKSSSRRAVNNHNSER-SMALLTIVIVVSVFLACWSP	258
QY	267	LEGLLADVFSSNLMACE--YLRGMDWILAVLANSANPIIYSPRSREVCRAVLSFCC	324
Db	259	LEIFELIDV---ACAKKCSLIFKSGWFMILAVLANSANPIYITLASKEMRAFFR-LVC	314
QY	335	GCLRIGMGPGDCLARAVEASGASTDSSCLRPDSFPGSRLSFRMRPLSSIS	380
Db	315	GCL--YVKGK-----TQASEMPALDPS--RSKSSSSNNSSHSPKXEDLPVAT	360
RESULT 8			
Q9PU08			
AC	Q9PU08	PRELIMINARY; PRT; 384 AA.	
DT	01-MAY-2000 (TREMBLrel. 13; Created)		
DT	01-MAY-2000 (TREMBLrel. 13; Last sequence update)		
DT	01-OCT-2001 (TREMBLrel. 18; Last annotation update)		
DE	EDG-3.		
GN	Edg-3.		
OS	Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;		
OC	Acanthomorphi; Acanthopterygii; Percomorpha; Tetraodontiformes;		
CC	Tetraodontidae; Takifugu.		
OX	NCBI_Taxid=31033;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=99439719; PubMed=10508926;		
RA	Yamauchi F., Yamauchi K., Tokuda M., Brenner S.;		
RT	"Molecular cloning of EDG-3 and N-She genes from the puffer fish, Fugu		
RT	rubripes, and conservation of synteny with the human genome."		
RL	FEBS Lett. 459:105-110(1999).		
DR	EMBL; AF161414; AAF07896.1; -.		
DR	InterPro: IPR004062; EDG3Rcdptor.		
DR	InterPro: IPR000276; GPCR_Rhodpsn.		
DR	InterPro: IPR004061; S1Preceptor.		
DR	Pfam; PF00001; 7tm1_1.		
DR	PRINTS; PRO1524; EDG3RECEPTOR.		
DR	PRINTS; PRO0237; GPCR_RHODOPSIN.		
DR	PRINTS; PRO1523; S1PRECEPTOR.		
DR	PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.		
DR	PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1		
SO	SEQUENCE 384 AA; 42712 MW; 92BDDF6BBD03BF CRC64;		
Query Match 32.6%; Score 640; DB 13; Length 384;			
Best Local Similarity 41.9%; Pred. No. 6.8e-44;			
Matches 147; Conservative 58; Mismatches 128; Indels 18; Gaps			
QY	24	LIVLHYNSGRLAGKGPEDS---GLGALRGLSVASC-LVYLENIVLAATTHMSRRSR	79
Db	6	LIVLHYNHYGKLDHR--PVGTSPTGRDPKTTAFIVYCSFIIENLTVLAIAWKNNRHN	63
QY	80	WYVYCVNTTSLDILTGAAYLANVLISGARTERFLPAQWFLREGLEFLTALAATSTFL	139
Db	64	RYVFFIGNALCDLLASAVIYLVNILLSGKTIQTLSPVLMFVREGSMFYILGASIPSLAI	123
QY	140	AGERPAWVRYAESGATKTSRVYGFGLCWLLAALLGMLPLGNNCLCAEDRCSSLLPL	199

[illegible]

OY 310 RSREVCRAVLSFLCCGCLRLGMRP 334
: : : : :
Db 310 TNRDLRHALLRLCCG-----RGP 328

RESULT 10
O91X56 PRELIMINARY; PRT: 400 AA.
AC O91X56;
DT 01-DEC-2001 (TREMblrel. 19, Created)
DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE Similar to sphingosine 1-phosphate receptor.
GN EDG8.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA Strausberg R.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC012332; AAH1232.1; -
DR MGI; MGI:2150641; Edg8.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PFO0001; 7tm_1; 1.
DR PRINTS; PR01561; EDG8RECEPTOR.
DR PROSITE; PS00337; G_PROTEIN_RECEPTOR_FL_1; UNKNOWN_1.
DR PROSITE; PS50262; G_PROTEIN_RECEPTOR_FL_2; 1.
KW Receptor.
SQ SEQUENCE 400 AA; 42330 MW; AA3118E8515F3F4 CRC64;

Query Match 32.3%; Score 636; DB 11; Length 400;
Best Local Similarity 41.9%; Pred. No. 1.5e-43;
Matches 153; Conservative 51; Mismatches 125; Indels 36; Gaps 8;

OY 22 SRLVLVHNHSGRLAGRGPEDEGIGALRLGSLVAASCLVLENLVLAAITSHMSRRMV 81
: : : : :
Db 12 SEVIVLVHNYTKLRGARVQPGAGLRADAACVLAFCATVLENLVLAVLHPRFHAPM 71
: : : : :
OY 82 YICLVNITISDLTGAAVYANVLSGARTFLAPQWFLREGSLFTALASTFSLFTAG 141
: : : : :
Db 72 FLLSLSTLSDLLAGAAVNTNLLSGPLTLRLSPALMFAREGGVVALAASVLSLALAL 131
: : : : :
OY 142 EEPATVVRVAESGATKTSRVYGFIGICMLAALLGMLPLGNNCLCAFDRCSLLPIXS 201
: : : : :
Db 132 EHLTLMAR-GRAPASARATLMAAVAMAGASLLGLPLAGMCLGRLETCTVLPPLA 190
: : : : :
OY 202 KRYILECLVIFAGVLAITMGLGATFRLVQASGQK-APRPAAR-----KARRL 249
: : : : :
Db 191 KAYVLECVLAFLGILAAICALYARLYCOVRANARLRAGPGSRRTSSRSRHTPRSLAL 250
: : : : :
OY 250 LKTVIMLLAFVLCGPIFLGILLADVFSGNMAQEYLGMDITLAVLNSAVNDIYSF 309
: : : : :
Db 251 LFTLSVLLAFVACGPIFLILLIDV-ACPARACPVLLQADPFGLAMANSILNIITYF 309
: : : : :
OY 310 RSREVCRAVLSFLCCGCLRLGMRP-----GDCLARAVEAHSAGS-----TTSSS 354
: : : : :
Db 310 TNRDLRHALLRLCCG-----RGPCNDSSNSLORSPSA-AGPSGGGLRRCCLPPTLDRS 362
: : : : :
OY 355 LRPRD 359
: : : : :
Db 363 SSPSE 367

RESULT 11
O99YN8 PRELIMINARY; PRT: 382 AA.
AC O99YN8; O99Y4;
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)

DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE G protein-coupled sphingolipid receptor (Hypothetical 42.8 kDa
protein) (EDG1).
GN CHEDG1 OR EDG1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN (1)
RP SEQUENCE FROM N.A.
RA Tigy1 G.U. Sr., Wang D. Sr.;
RT "Correction to Human EDG1 sequence."
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
RN (2)
RP SEQUENCE FROM N.A.
RC TISSUE=LUNG;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
RN (3)
RP SEQUENCE OF 41-366 FROM N.A.
RX MEDLINE-21082082; PubMed-11214319;
RA Murphy W.J., Elizirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
O'Brien S.J.;
RL "Molecular phylogenetics and the origins of placental mammals."
DR EMBL; AF233365; AAF43420.1; -
DR Nature 409:614-618(2001).
DR EMBL; BC018650; AAH18650.1; -
DR EMBL; AY011725; AAK01993.1; -
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR InterPro; IPR004061; S1PReceptor.
DR Pfam; PFO0001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHOOPSN.
DR PRINTS; PR01523; S1PRECEPTOR.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR_FL_1; UNKNOWN_1.
DR PROSITE; PS50262; G_PROTEIN_RECEPTOR_FL_2; 1.
KW Hypothetical protein; Receptor.
SQ SEQUENCE 382 AA; 42810 MW; 0CCE8685A5E1BAD2 CRC64;

Query Match 32.3%; Score 635.5; DB 4; Length 382;
Best Local Similarity 40.5%; Pred. No. 1.6e-43;
Matches 136; Conservative 64; Mismatches 121; Indels 15; Gaps 6;

OY 1 MNATGTVAPESCCOLAAGSHRLVLYHNHSGRLAGRGPEDEGIGALRLGSLVAASCLV 60
: : : : :
Db 1 MGPTSVPLVAHRSVSDVYNDIVHNYTKL-NISADKNSIKLSVIFLLCCFI 59
: : : : :
OY 61 VLENLVLAAITSHMSRRRVYICLVNITISDLTGAAVYANVLSGARTFLAPQWFL 120
: : : : :
Db 60 ILENIFVLITITWKTKFHRPMYFYGMLALSDLAGAAVYANLILSGATFYKLPQWFL 119
: : : : :
OY 121 REGILFTALASTFSLFTAGEFATVVRVAESGATKTSRVYGFIGICMLAALLGMLP 180
: : : : :
Db 120 REGSMFVALNASVPSLALITERYITMLKKKLNIG-SNNRFLVLLSACVVISLILGLP 178
: : : : :
OY 181 LIGNNICAFDRCSLLPIYSKRYILECLVIFAGVLAITMGLGATFRLVQASGQ----- 235
: : : : :
Db 179 IMGNCISALSSCSSTVPLVHKHYILECTVFTLLLSITVLCRIYSLVTRSRRLTR 238
: : : : :
OY 236 ----KARPPARKARRLKTVIMLLAFVLCGPIFLGILLADVFSGNMAQEYLGMDM 291
: : : : :
Db 239 KNISKASR--SSEKSLALPTIIVISVFTACWAPFILLIDV-GCKVKTCDILPRAEY 295
: : : : :
OY 292 ILALAVLSAVNPPIYSFRSREVCRAVLSFL-CCGC 326
: : : : :
Db 296 FLVLAIVNSGNTPIITITTKKERRAFIRIMSCCK 331

RESULT 12
O99MN8 PRELIMINARY; PRT: 387 AA.
AC O99MN8;
DT 01-JUN-2001 (TREMblrel. 17, Created)
DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)

